

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

FIG. 1A

HEME BIOSYNTHESIS

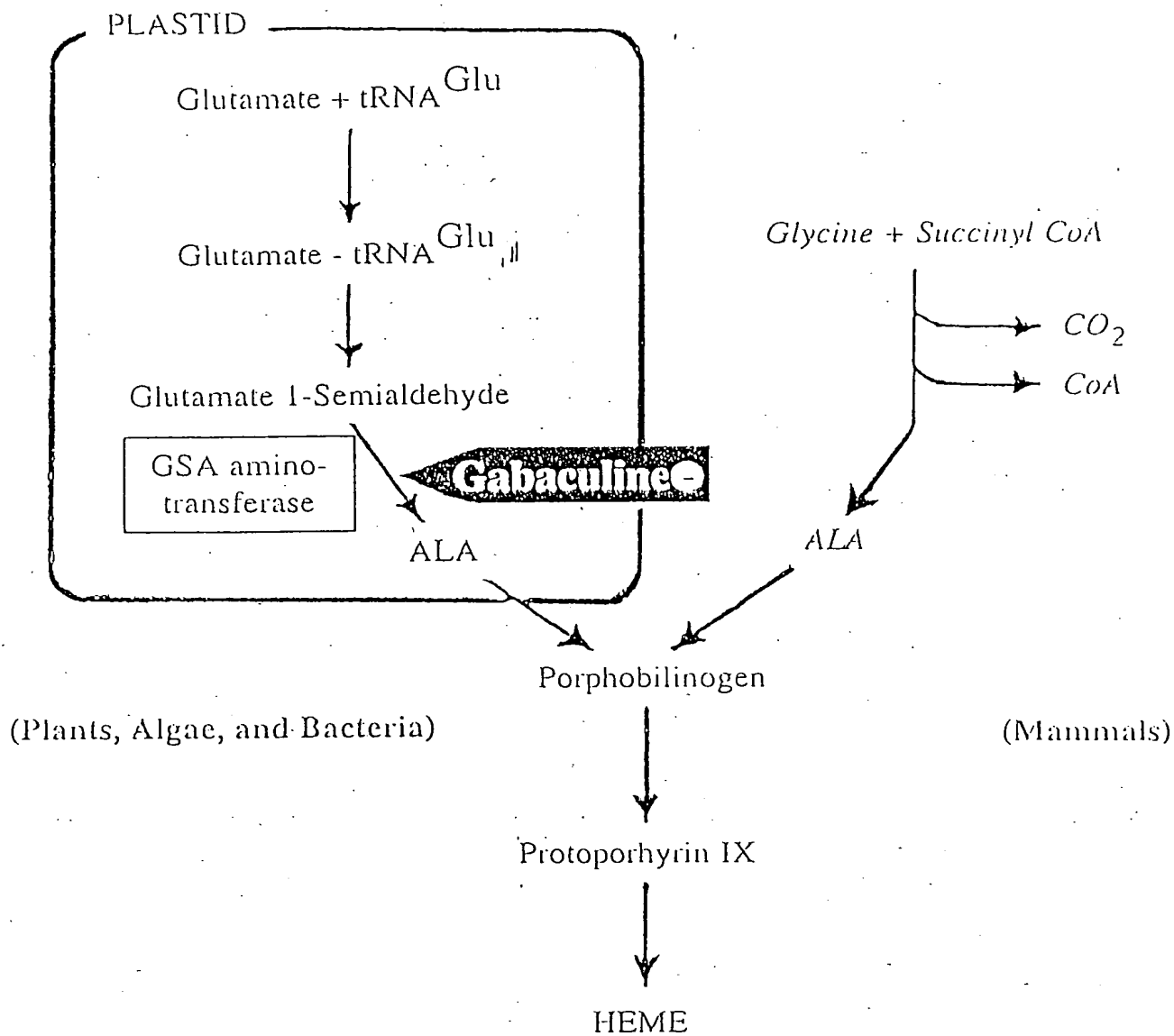


FIG. 1B

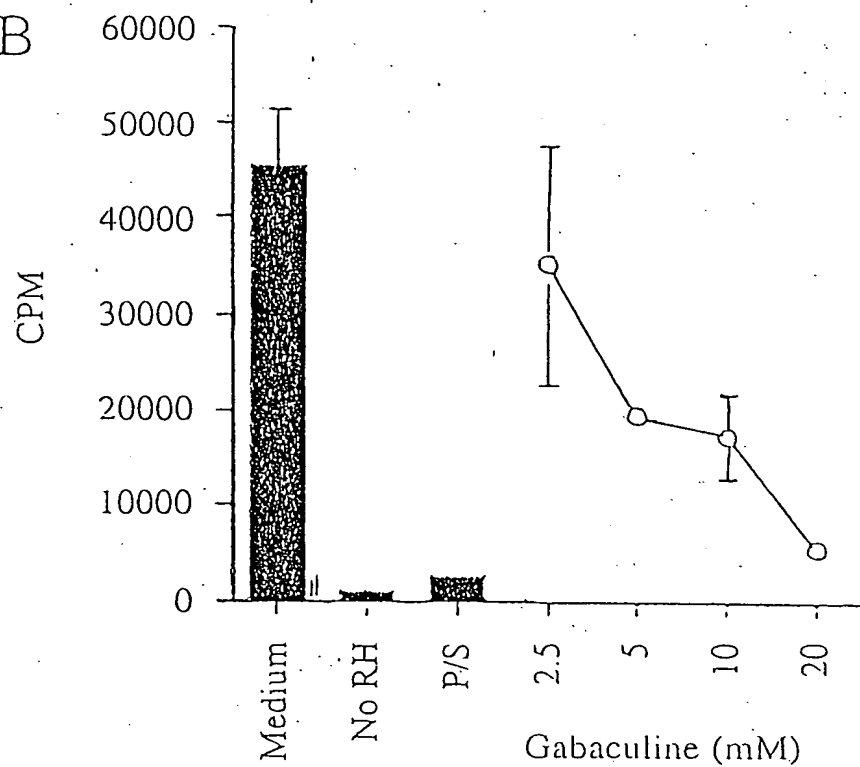


FIG. 1C

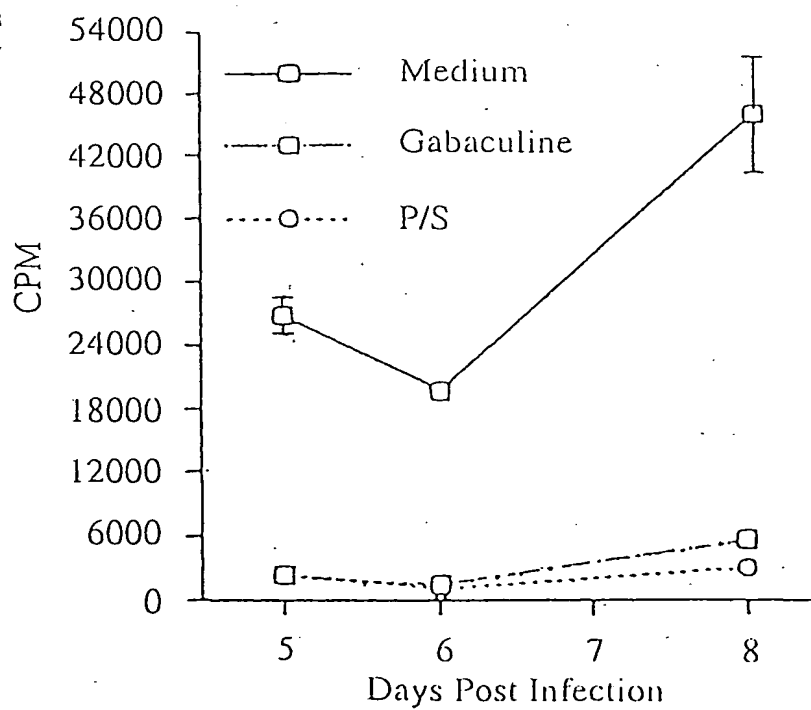


FIG. 2A

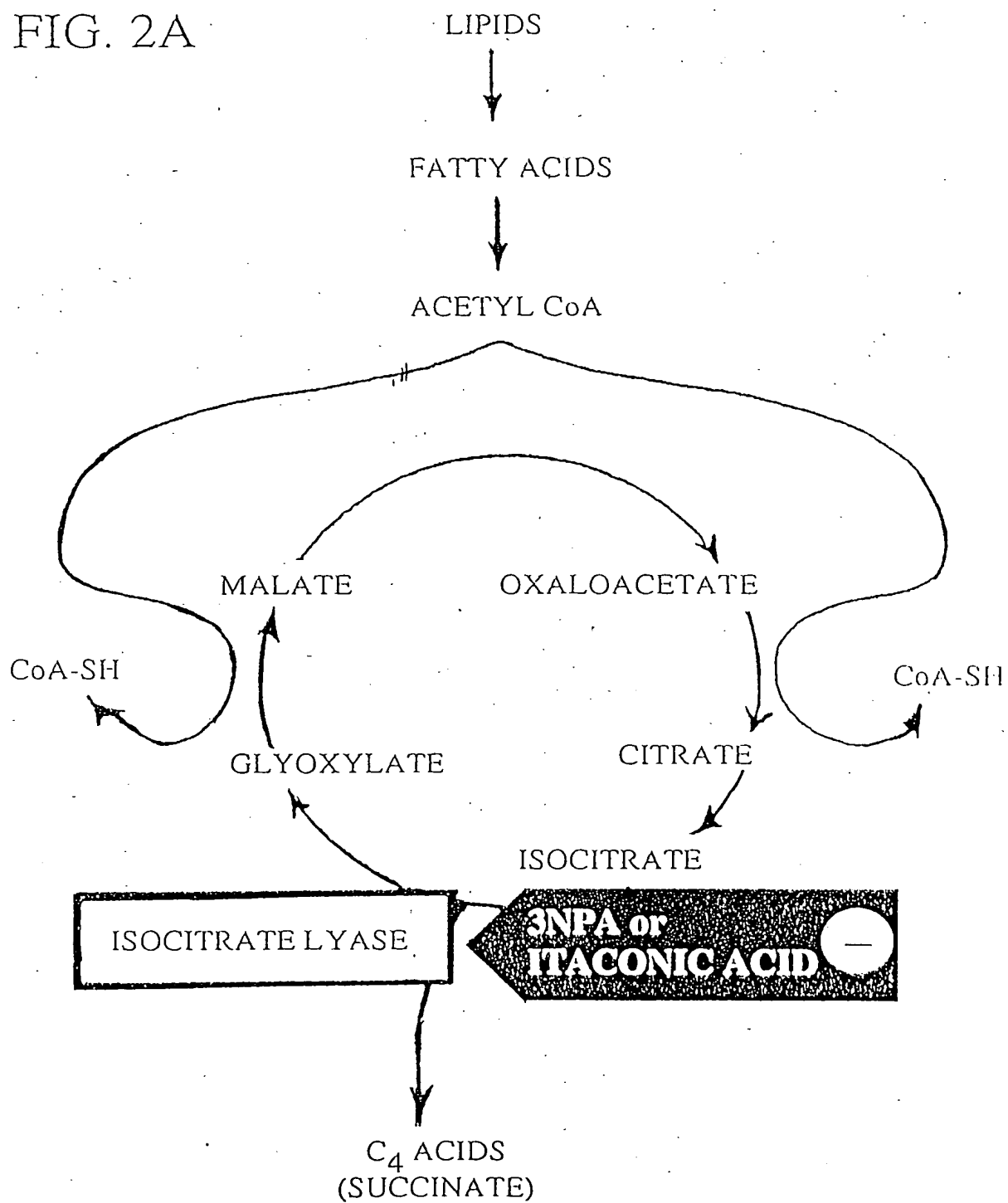


FIG. 2B

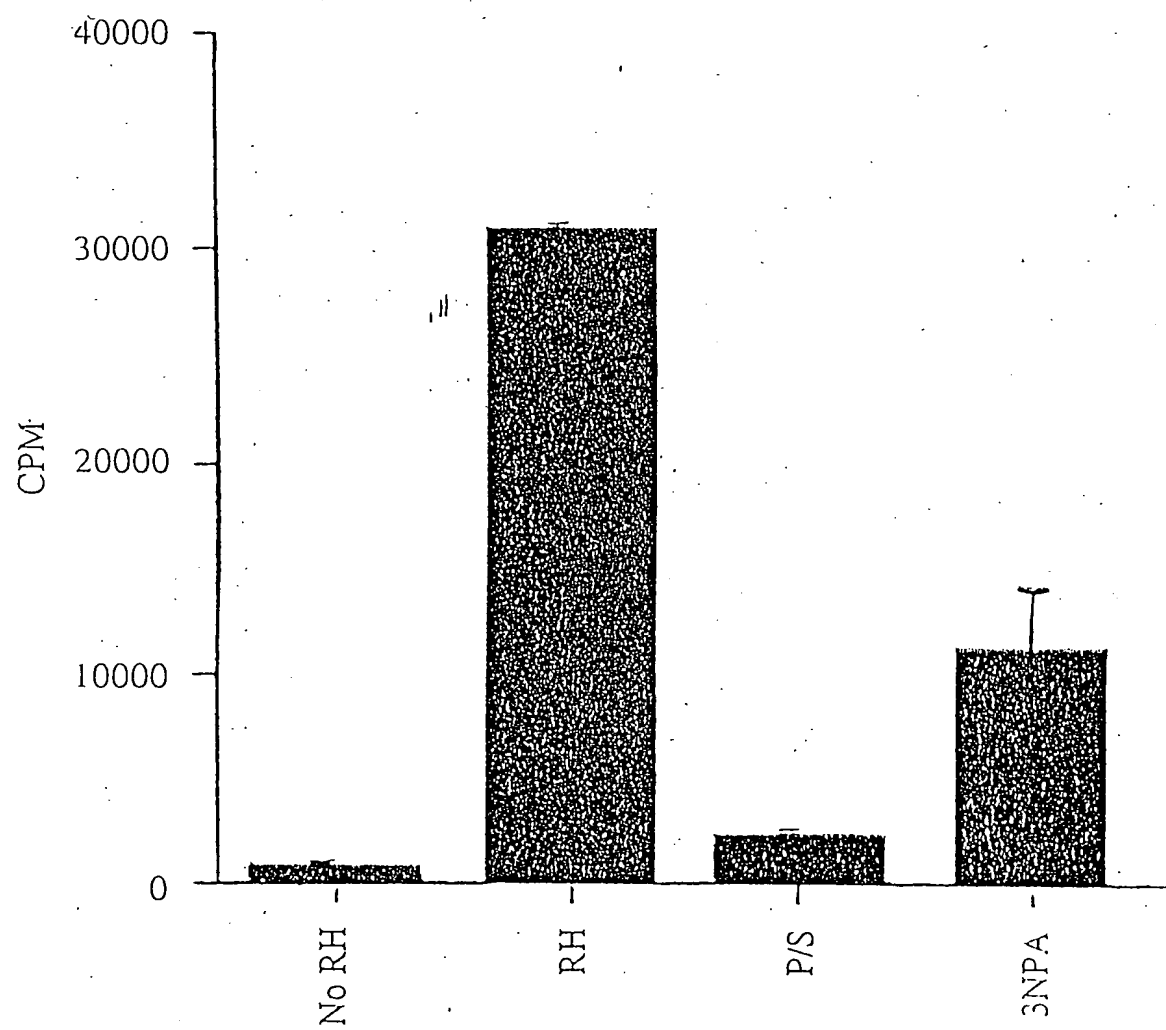


FIG. 3A

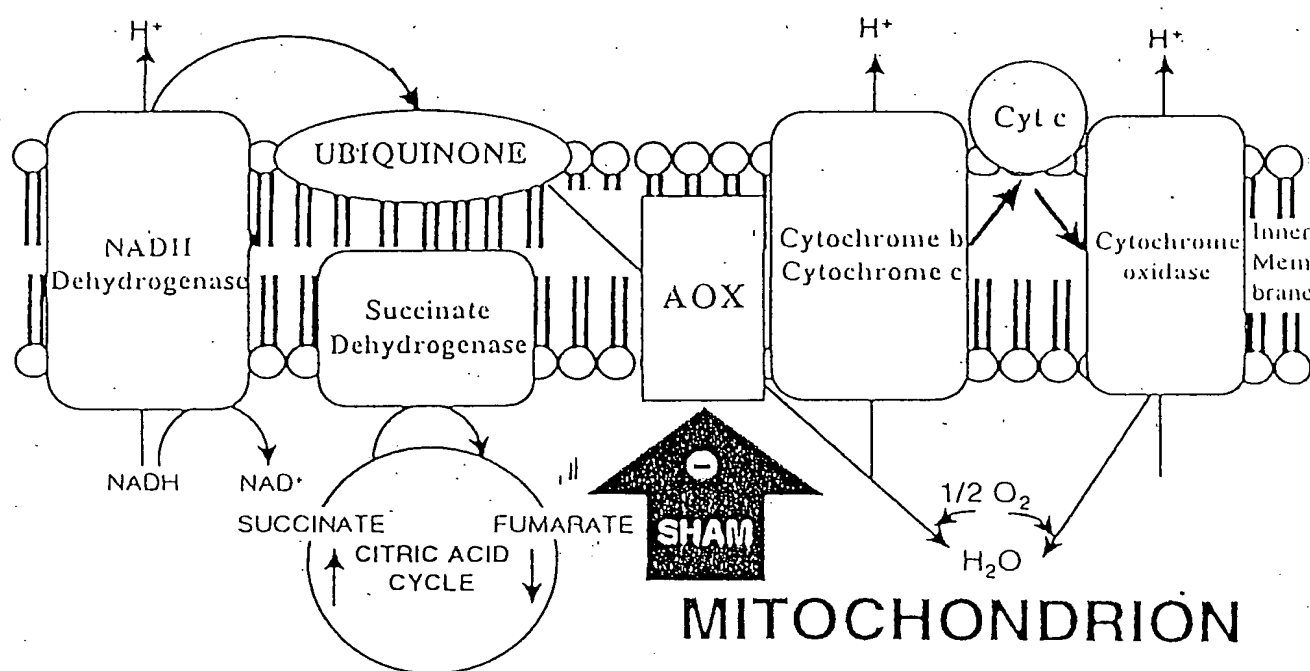


FIG. 3B

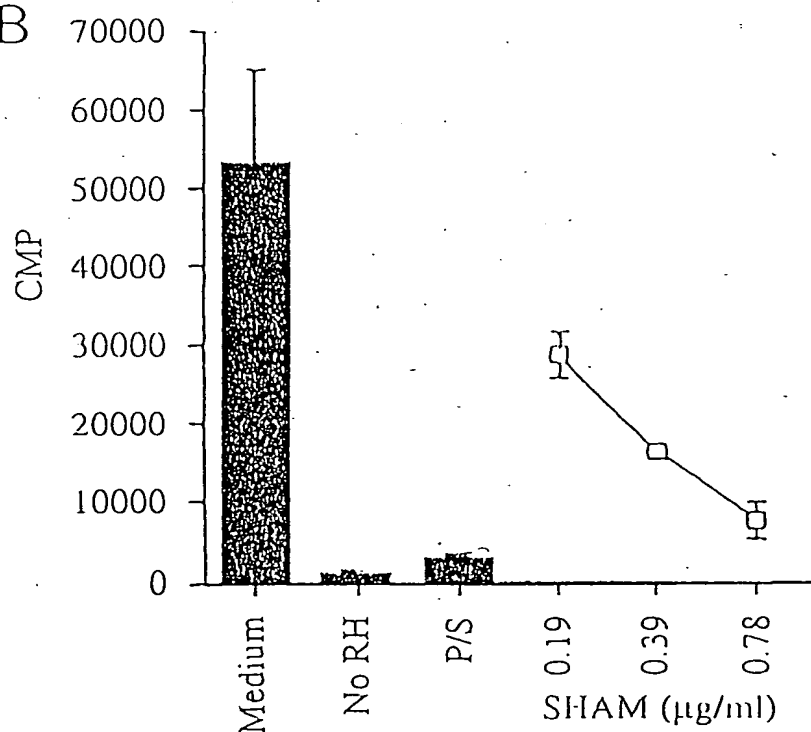


FIG. 4A

PHOSPHOENOLPYRUVATE + ERYTHROSE 4-PHOSPHATE

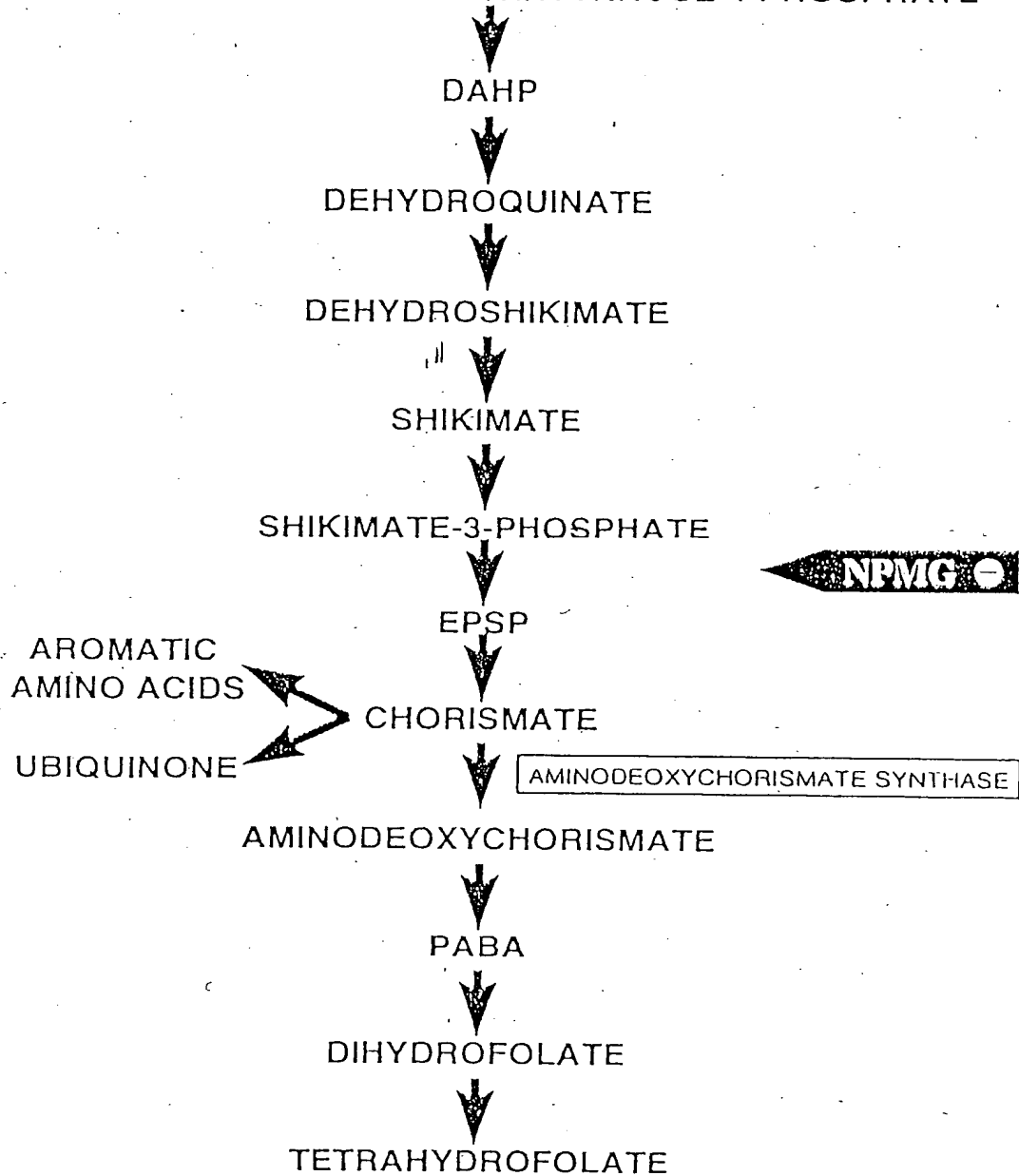


FIG. 4B

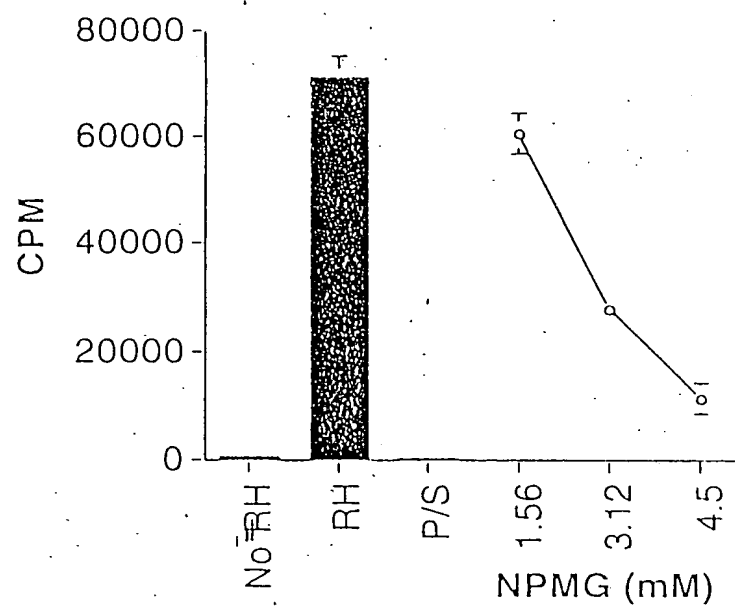


FIG. 4C

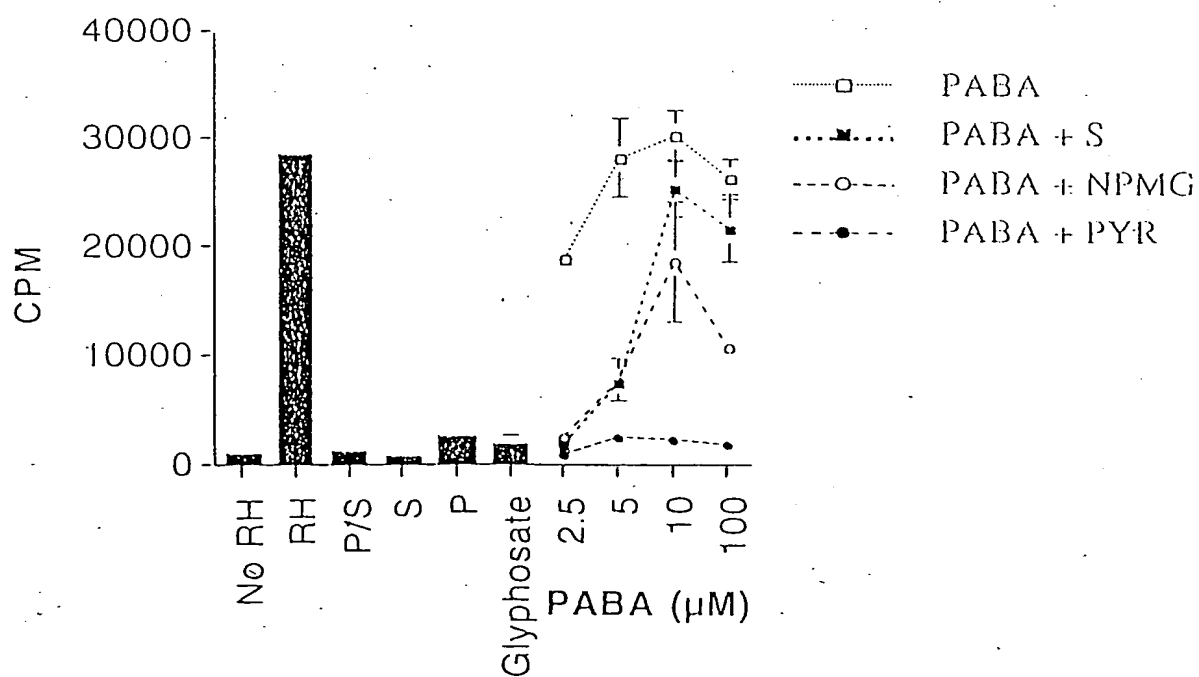


FIG. 4D

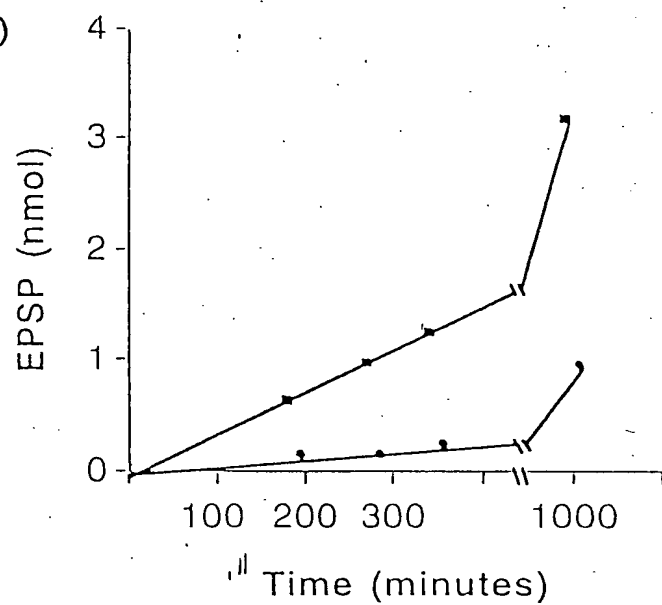


FIG. 4E

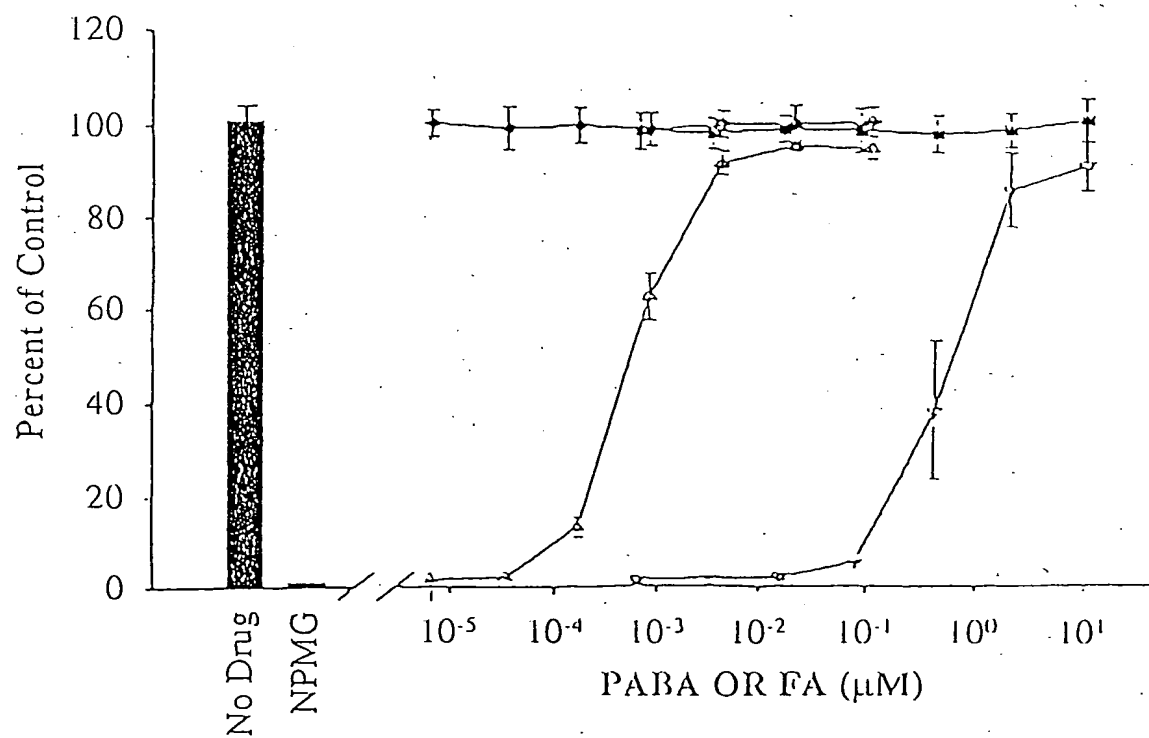


FIG. 5

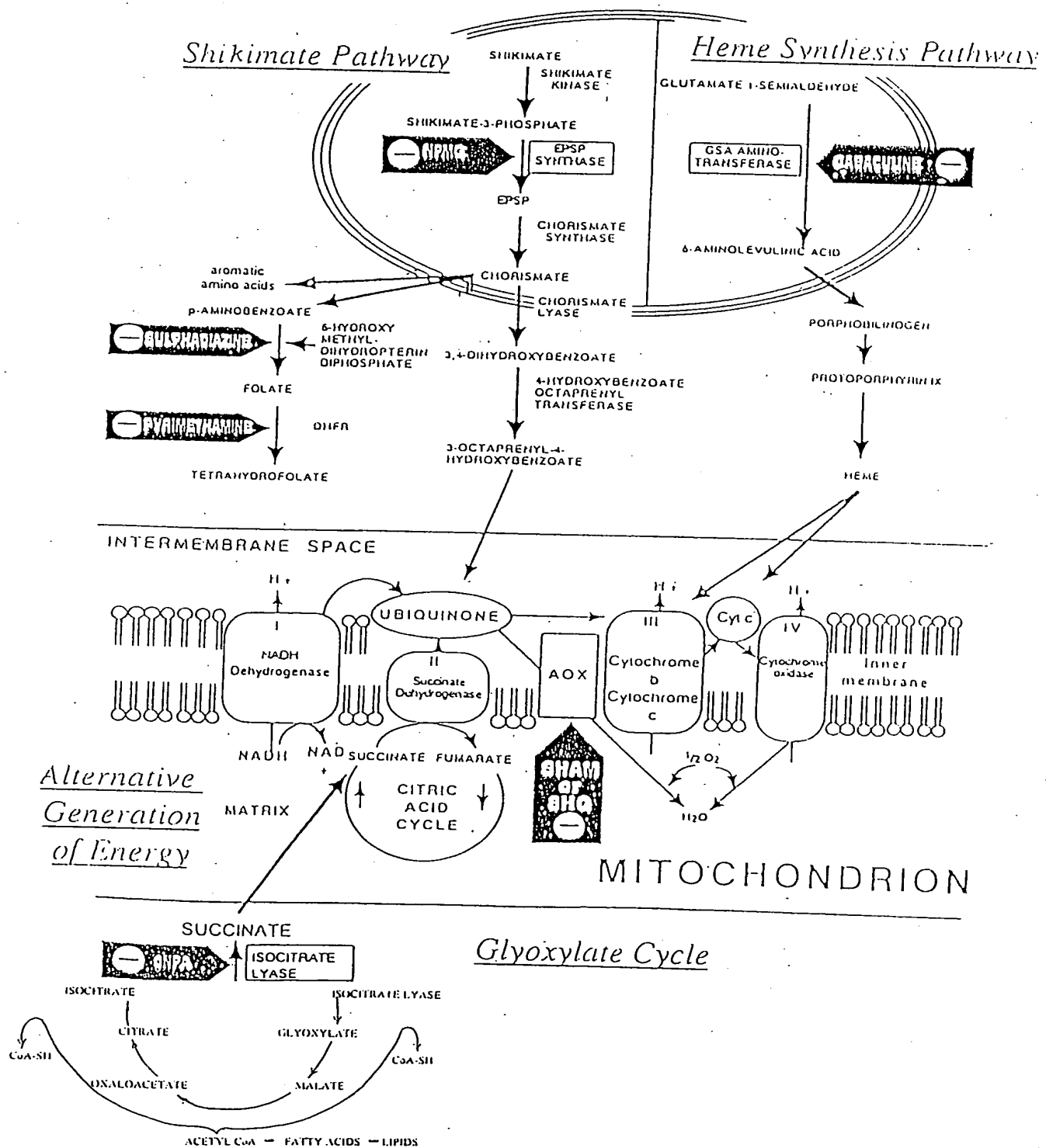


FIG. 6

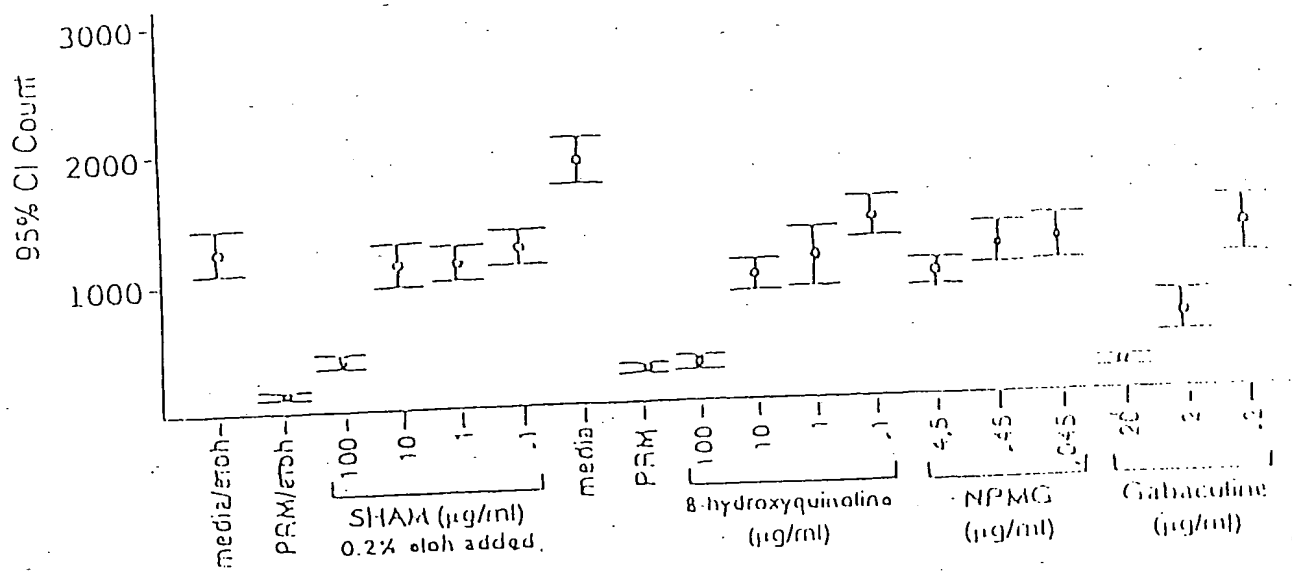


FIG. 7

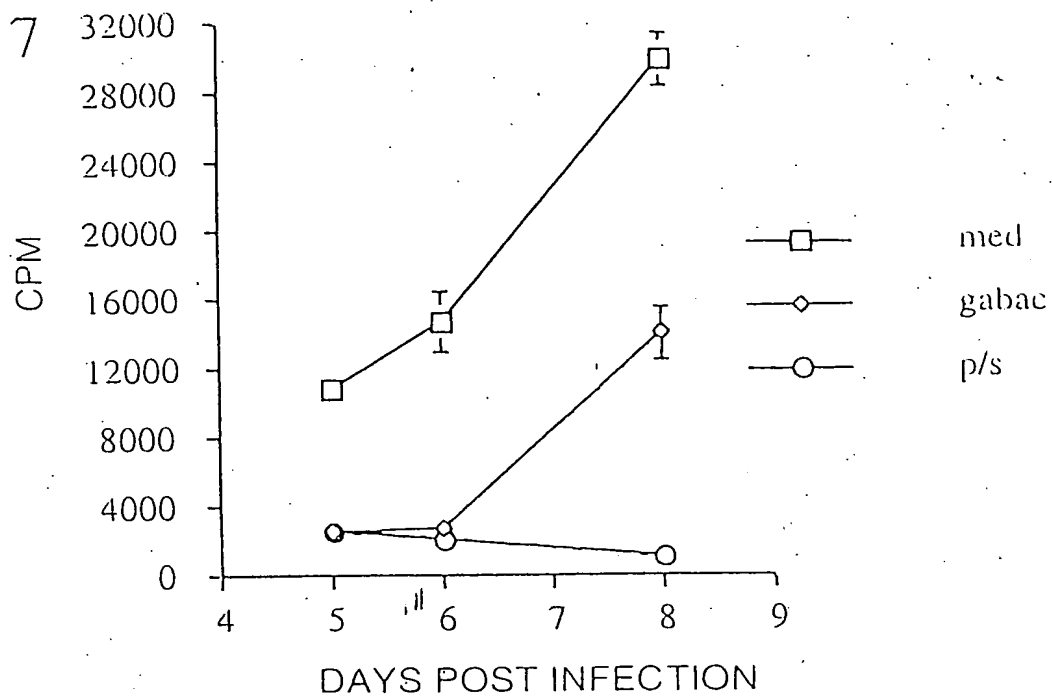


FIG. 8

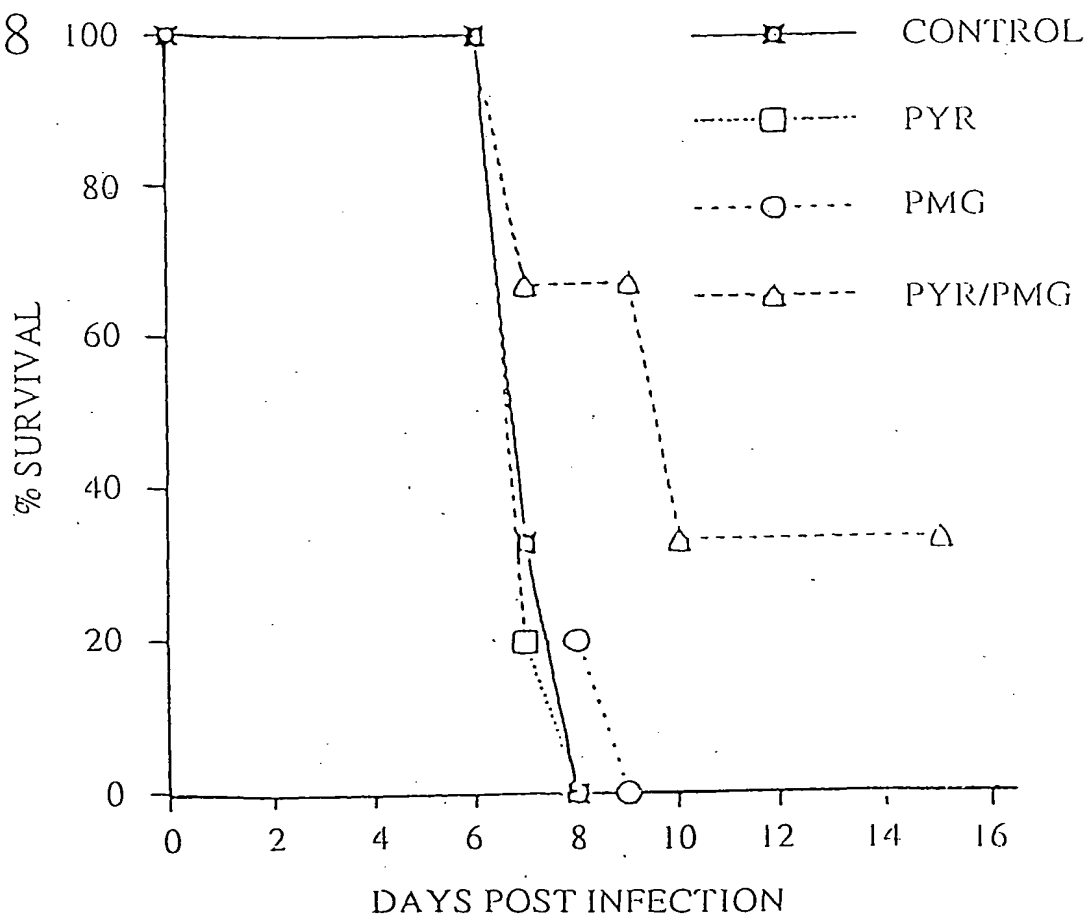


Fig. 9(1)

	CT	CAT	CTT	CTC	GGT	TTC	17									
ACT	TTT	CTT	TGA	GTG	CCT	GTG	TGA	GAG	ACG	GTC	GTC	GCA	ACA	AGA	ATC	65
TCC	TCC	GCT	CAC	GCC	TTT	CCT	CAC	AGT	CCT	GTT	TTT	CCT	CCA	GCT	GTC	113
ACA	CAT	CCC	GCT	CGT	TCC	GCT	GCA	TCT	CCT	CAC	ATT	TCT	TGC	AGT	CAG	161
ATG	TCT	TCC	TAT	GGA	GCC	GCT	CTG	CGC	ATA	CAC	ACT	TTC	GGT	GAA	TCT	209
M	S	S	Y	G	A	A	L	R	I	H	T	F	G	E	S	16
CAC	GGC	TCA	GCC	GTT	GGG	TGT	ATA	ATC	GAC	GGG	CTG	CCT	CCT	CGC	CTC	257
H	G	S	A	V	C	C	I	I	D	G	L	P	P	R	L	32
CCT	CTT	TCT	GTC	GAA	GAT	GTT	CAG	CCT	CAA	TTA	AAT	CGC	AGA	AGA	CCC	305
P	L	S	V	E	D	V	Q	P	Q	L	N	R	R	R	P	48
GGC	CAA	GGG	CCT	CTC	TCG	ACG	CAG	CGG	AGA	GAG	AAA	GAT	CGA	GTC	AAC	353
G	Q	G	P	L	S	T	Q	R	R	E	K	D	R	V	N	64
ATA	CTC	TCC	GGT	GTT	GAA	GAT	GGA	TAT	ACA	CTC	GGT	ACT	CCC	CTG	CGC	401
I	L	S	G	V	E	D	G	Y	T	L	G	T	P	L	A	80
ATG	CTC	GTC	TGG	AAT	GAA	GAC	CGG	CGG	CCC	CAG	GAA	TAC	CAC	GCC	CTC	449
M	L	V	W	H	E	D	R	R	P	Q	E	Y	H	A	L	96
GCG	ACA	GTC	CCG	CGT	CCA	GGT	CAC	GGG	GAT	TTC	ACC	TAC	CAT	GCA	AAG	497
A	T	V	P	R	P	G	H	G	D	F	T	Y	H	A	K	112
TAC	CAC	ATT	CAC	CGC	AAA	AGC	GGG	GGC	GGT	CGG	AGC	AGC	GCG	CGG	GAG	545
Y	H	I	H	A	K	S	G	G	G	R	S	S	A	R	E	128
ACT	TTG	GCG	CGC	GTC	GCC	GCT	GGA	GCA	GTC	GTT	GAG	AAG	TGG	CTA	GGC	593
T	L	A	R	V	A	A	G	A	V	V	E	K	W	L	G	144
ATG	CAC	TAC	GGC	ACC	AGC	TTC	ACA	GCT	TGG	GTC	TGT	CAG	GTT	GGT	GAT	641
H	H	Y	G	T	S	F	T	A	W	V	C	Q	V	G	D	160
GTC	TCT	GTG	CCC	CGA	TCG	CTC	CGA	AGA	AAG	TGG	GAG	CGG	CAG	CCG	CCA	689
V	S	V	P	R	S	L	R	R	K	W	E	R	Q	P	P	176
ACT	CGC	CAA	GAC	GTC	GAT	CGC	CTT	GGC	GTG	GTC	CGC	GTG	AGC	CCA	GAT	737
T	R	Q	D	V	D	R	L	G	V	V	R	V	S	P	D	192
GGA	ACC	ACA	TTT	CTC	GAC	GCG	AAC	AAC	CGC	CTT	TAC	GAC	GAG	CGA	GGA	785
G	T	T	F	L	D	A	N	N	R	L	Y	D	E	R	G	208
GAG	GAA	CTC	GTC	GAG	GAG	GAA	GAC	AAA	GCC	AGG	CGT	CGG	CTT	CTT	TTC	833
E	E	L	V	E	E	E	D	K	A	R	R	R	L	L	F	224
GGA	GTC	GAC	AAC	CCG	ACG	CCA	GGA	GAA	ACA	GTG	ATT	GAG	ACC	AGG	TGC	881
G	V	D	N	P	T	P	G	E	T	V	I	E	T	R	C	240
CCG	TGC	CCC	TCC	ACA	GCT	GTT	CGC	ATG	GCT	GTG	AAA	ATC	AAC	CAG	ACC	929
P	C	P	S	T	A	V	R	H	A	V	K	I	N	Q	T	256
CGA	TCT	CTG	GSC	GAT	TCG	ATT	GGC	GGA	TGC	ATC	TCC	GGT	GCA	ATC	CTG	977
R	S	L	G	D	S	I	G	G	C	I	S	G	A	I	V	272
CGG	CCA	CCG	CTG	GGC	CTC	GGC	GAG	CCG	TGT	TTC	CAC	AAA	GTG	GAG	GGG	1025
R	P	P	L	G	L	G	E	P	C	F	D	K	V	E	A	288
GAG	CTG	CCG	AAG	GCG	ATG	ATG	TCC	CTC	CCT	GCT	ACG	AAA	GGG	TTT	GAG	1073
E	L	A	K	A	M	M	S	L	P	A	T	K	G	F	E	304
ATT	GGC	CAG	GGC	TTT	GCG	AGT	GTC	ACG	TTG	CGA	GGC	AGC	GAG	CAC	AAC	1121
I	G	Q	G	F	A	S	V	T	L	R	G	S	E	H	H	320
GAC	CGC	TTC	ATT	CCC	TTC	GAG	AGA	GCG	TCG	TGT	TCA	TTC	TCG	GAA	TCA	1169
D	R	F	I	P	F	E	R	A	S	C	S	F	S	E	S	336
GCC	GCG	AGC	ACG	ATC	AAG	CAT	GAA	AGA	GAT	GGG	TGT	TCA	GCT	GCT	ACA	1217

TO FIG. 9(2)

[illegible]

Fig. 9(2)

Fig. 10 (1)

T. gondii	-----MSSYGAALRIH	11
Synechocystis	-----HGNTFGSLFRIT	12
S. lycopersicum	MASSHLTKQFLGAPFSSFGSQQPSKLCSSHLRFPTHRSQPKRLEIQAGNTFGNYFRVT	60
N. crassa	-----MSTFGHYFRVT	11
H. influenza	-----MAGNTICQLFRVT	13
S. cerevisiae	-----MSTFGKLFRT	11
T. gondii	TFGESHGSAVGGCIIDGLPPRLPLSVEDVQPQLNRRRPGQGPLSTQRREKDRVNIISGVED	71
Synechocystis	TFGESIHGGGVGVIIIDGCPRLLEISPEEIQVDLDRRRPGQSKIITPRKEADQCEILSGVFE	72
S. lycopersicum	TFGESIHGGGVGGCIIDGCPRLPLSESDMQVELDRRRPGQSRITTPRKETDTCKISSGTAD	120
N. crassa	TYGESHCCKSVGGCIVDGVPPHCHMELTEDDIQPHTRRRPGQSAITTPRDEKDRVI IQSGTEF	71
H. influenza	TFGESHGIALGCIVDGVPPNLELSEKDIQPOLDRRKPGTSRYTTPRREDDEVQILSGVFE	73
S. cerevisiae	TYGESHCCKSVGGCIVDGVPPGMSLLEADIQPOLTRRRPGQSKLSTPRDEKDRVE IQSGTEF	71
T. gondii	GYTLGTPLAMLVNEDRRPQEH--ALATVPRPGHGDFTYHAKYHIIAKSGGGRSSARET	129
Synechocystis	GKTLGTPIAILVRNKDARSQDYN--ENAVKYRPSHADATYEAKYGIIRIMQGGGRSSARET	130
S. lycopersicum	GLTTGSPIKVEVPNTDQRGNDS--EHSLAYRPSHADATYDFKYGVRSVQGGGRSSARET	178
N. crassa	GVTLTGTPIGHLVNEDQPPKDYGNKTMIDIYRPSHADWTYLEKYGVKASSGGGRSSARET	131
H. influenza	GKTTGTSIGHIINQDQRSQDYG--DIKDRFRPGHADFTYQQKYGIROYRGGGRSSARET	131
S. cerevisiae	GKTLGTPIANHIKNEDQRPHOYS--DMDKFRPSHADFTYSEKYGIKASSGGGRASARET	129
T. gondii	LARVAAGAVVEKHLGHYGTSTAWVCQVGDVSVPRSLRRKWERQPTRQDVDRLGVVVRV	189
Synechocystis	IGRVAAGATAKKILAQFNGVEIVAYVKS IQDIEA-----	164
S. lycopersicum	IGRVAAGAVAKKILKLYSGTEILAYVSQVIIMVLP-----	213
N. crassa	IGRVAAGATAEKYLKPRYGVIEIVAFVSSVSGSEHL7PPTAEHPSPST-----	177
H. influenza	AMRVAAGATAKKYLREHFGIEVRGFLSQIGNIKIAP-----	167
S. cerevisiae	IGRVASGATAEKFLAQNSHVEIVAFVTQIGFIKHIR-----	165
T. gondii	SPDGTTFLOANRLYDERGEELVEEEDKARRRLLEFGVDNPTPGETV IETRCPCPSTAVRH	249
Synechocystis	-----TVDSNTVTLEQVESN-----IVRCPDEECAEFH	192
S. lycopersicum	-----EDLVDMQIVTLEQIESN-----IVRCPHPEYAEKH	243
N. crassa	-----NPEFLKLVNSITRETVDOSFL-----PVRCPDAEANKRH	210
H. influenza	-----QKVGQIDWEKVNSN-----PFFCPDESAREKF	194
S. cerevisiae	DSFDPEFQILLNTITREKVDSHG-----PIRCFDASVAGLM	201
T. gondii	AVKIHQTRSLGDSIGGCISGAIVRPPLGLGEPFDFVEAELAKAMHSLPATKGF EIGQGF	309
Synechocystis	IERIDQVLRQKDSIGGVVECAIRHAPKGLGEPVFDKLEADLAKAMHSLPATKGF EFGSGF	252
S. lycopersicum	IGADIVVRVRCDSVGGVVTICVRNVPRGLGTPVFDKLEAELAKACHSLPATKGF EFGSGF	303
N. crassa	EDLITKFRDNHDSIGCTVTCVIRNVPSGLGEPAFDKLEAHIAHLSIPATKGF EFGSGF	270
H. influenza	DELIRELKKEGDSIGAKLTVIAENVVGLGEPVFORLDADLAHALMGINAVKGV EIGDGF	254
S. cerevisiae	VKEIEKYRGKDSIGGVVTCVVRNLPTGLGEPFDFKLEAHIAHLSIPASEGF EIGSGF	261

TO FIG. 10 (2)

— TO FIG. 10(1) —

T.gondii	ASVTLRGSEIWDRFIPFERASCSFSESAASTIKHERDGC SAATLSRERASDGRITTSRHEE	169
Synechocystis	AGTLLTGSQHND EYYIDEAGEWR-----	275
S.lycopersicum	AGTFMTGSEHNDEFFMDEHDQIR-----	326
N.crassa	GGCEVPGSIHNDPFVSAENTEIPPSVAASGAARNGI-----	306
H.influenza	AVVEQRGSEHRDEMTPNGFESNH-----	277
S.cerevisae	QGVSVPGSKINDPFYFEKETNR-----	283

T.gondii	EVERGRERIQRDTLIIVTGVDQONGNSED SVRYTSKSEASITRLSGNAASGGAPVCRIPLG	429
Synechocystis	-----	
S.lycopersicum	-----	
N.crassa	-----	
H.influenza	-----	
S.cerevisae	-----	

T.gondii	EGVRIRCGSHMAGGTLAGITSGENIFFRVAFKPVSSIGLEQETADFA-GENHQLAVKGRH	400
Synechocystis	-----TRTNRSGGVQGGISNGEPIIHRIAFKPTATIGQEOKTVSMI-GEETTLAAKGRH	328
S.lycopersicum	-----TKTNRSGGIQGGISNGEIIHNRVAFKPTSTIARKQHTVSRD-KHETELIARGRH	379
N.crassa	PRPKLTTKTNFSGGIQGGISNGAPIYFRVGFKPAATIGQEQTATYDGTSEGVLAAGRH	366
H.influenza	-----ACGILGGISSQPIIATIALKPTSSITIPGRSINLH-GEAVEVTKGRH	325
S.cerevisae	-----LRTKTNNSGGVQGGISNGENIYFSVPFKSVATISQEOKTATYD-GEEGI LAAGRH	330

T.gondii	DPCVLPRAPPLVESMAALVIGDLCLQRAREGPHLLVLPQHSGCPSC-----	536
Synechocystis	DPCVLPRAVPHVEAMAALVLCPIHLLRFQAQCKTL-----	362
S.lycopersicum	DPCVVPRAVPHVEAHVALVLVDQLMTQYAQCHLFPVNLTLQEPLQPSTTKSA-----	431
N.crassa	DPSVVPRAVPIVENMAALVIHDAVLNIARVTAKSLLPLKQTINSCKDTVGHGVSEHVQ	426
H.influenza	DPCVGIRAVPIAEAHVAIVLLOHLLRFKAQCK-----	357
S.cerevisae	DPAVTPRAIPIVEAHVALVLADALLIQKARDFSRSVH-----	376

T.gondii	-----	
Synechocystis	-----	
S.lycopersicum	-----	
N.crassa	ESDLAQ	432
H.influenza	-----	
S.cerevisae	-----	

Fig. 10(2)

processing site

(SEQ ID NO: 44)

(SEQ ID NO: 43)

SCSPSESANSTINKIERDCSANTLSRASPDRTSRHEEVERG

Fig. 11.

Fig. 12 (1)

McLeod *et al.*

CT CGA GTT															8	
TTT	TTT	TTT	TTT	TTT	TTT	TTG	ATA	CAT	AAT	AAT	CAA	GAG	TTC	TTT	ATA	52
CTA	ACA	GAC	TTA	TTT	AAT	GTA	TTA	TTT	TTG	GTA	AAC	AAA	AAA	AAC	ATT	104
ATG	AGC	ACA	TAT	GGG	ACT	TTA	TTA	AAA	GTA	ACA	TCC	TAC	GGA	GAA	AGT	152
M	S	T	Y	G	T	L	L	K	V	T	S	Y	G	E	S	16
CAT	GGG	AAA	GCT	ATT	GGG	TGT	GTG	ATC	GAT	GGG	TTT	TTA	TCC	AAT	ATA	200
H	G	K	A	I	G	C	V	I	D	G	F	L	S	N	I	32
GAA	ATA	AAT	TTT	GAT	TTA	ATA	CAA	AAA	CAA	TTA	GAT	AGA	CGA	AGA	CCA	248
E	I	N	F	D	L	I	Q	K	Q	L	D	R	R	R	P	48
AAT	CAA	TCA	AAA	CTA	ACT	AGT	AAT	AGA	AAC	GAA	AAA	GAT	AAA	CTT	GTT	296
N	Q	S	K	L	T	S	N	R	N	E	K	D	K	L	V	64
ATA	CTT	TCA	GGA	TTT	GAT	GAA	AAT	AAA	ACA	TTA	GGT	ACA	CCT	ATT	ACA	344
I	L	S	G	F	D	E	N	K	T	L	G	T	P	I	T	80
TTT	TTA	ATA	TAT	AAT	GAA	GAT	ATT	AAA	AAA	GAA	GAT	TAT	AAT	TCT	TTT	392
F	L	I	Y	N	E	D	I	K	K	E	D	Y	N	S	F	96
ATA	AAT	ATT	CCT	AGA	CCA	GGA	CAT	GGA	GAT	TAT	ACC	TAT	TTT	ATG	AAA	440
I	N	I	P	R	P	G	H	G	D	Y	T	Y	F	M	K	112
TAT	CAT	GTT	AAA	AAT	AAA	AGT	GGA	AGT	AGT	AGA	TTT	TCT	GGA	AGA	GAA	488
Y	H	V	K	N	K	S	G	S	S	R	F	S	G	R	E	128
ACA	GCC	ACA	AGA	GTT	GCT	GCT	GGG	GCG	TGC	ATT	GAA	CAA	TGG	CTT	TAT	536
T	A	T	R	V	A	A	G	A	C	I	E	Q	W	L	Y	144
AAA	TCT	TAT	AAT	TGT	TCT	ATT	GTT	AGT	TAT	GTA	CAT	TCA	GTT	GGG	AAT	584
K	S	Y	N	C	S	I	V	S	Y	V	H	S	V	G	N	160
ATA	AAG	ATA	CCT	GAA	CAA	GTC	AGC	AAA	GAA	TTG	GAA	AAT	AAA	AAT	CCA	632
I	K	I	P	E	Q	V	S	K	E	L	E	N	K	N	P	176
CCC	TCA	AGA	GAT	TTA	GTA	GAT	TCT	TAT	GGA	ACC	GTT	AGA	TAT	AAT	GAA	680
P	S	R	D	L	V	D	S	Y	G	T	V	R	Y	N	E	192
AAA	GAA	AAA	ATA	TTT	ATG	GAT	TGT	TTT	AAT	AGA	ATA	TAT	GAT	ATG	AAT	728
K	E	K	I	F	H	D	C	F	N	R	I	Y	D	M	N	208
GCT	TCT	ATG	TTA	AAA	ACT	GAT	GAA	TAT	AAT	AAA	AAC	ACA	TTG	ACT	ATT	776
A	S	M	L	K	T	D	E	Y	N	K	N	T	L	T	I	224
CCT	TCA	ATA	GAT	AAC	ACG	TAT	ATA	AAT	GTA	AAA	ACT	AAT	GAA	TGT	AAT	824
P	S	I	D	N	T	Y	I	N	V	K	T	N	E	C	N	240
ATA	AAT	CAG	GTT	GAT	AAT	AAT	CAT	AAC	AAT	TAT	ATT	AAT	GAT	AAG	GAT	872
I	N	Q	V	D	N	N	H	N	N	Y	I	N	D	K	D	256
AAC	ACT	TTT	AAT	AAT	TCT	GAA	AAA	TCG	GAT	GAA	TGG	ATT	TAT	TTA	CAA	920
H	T	F	N	N	S	E	K	S	D	E	W	I	Y	L	Q	272
ACA	AGA	TGT	CCA	CAT	CCA	TAT	ACT	GCT	GTA	CAA	ATT	TGT	TCT	TAT	ATT	968
T	R	C	P	H	P	Y	T	A	V	Q	I	C	S	Y	I	288
TTG	AAA	CTA	AAA	AAT	AAA	GGA	GAT	ACT	GTT	GGG	GGT	ATT	GCT	ACA	TGC	1016
L	K	L	K	N	K	G	D	S	V	G	G	I	A	T	C	304
ATT	ATA	CAA	AAT	CCT	CCT	ATA	GGT	ATT	GGA	GAA	CCT	ATT	TTT	GAC	AAA	1064
I	I	Q	H	P	P	I	G	I	G	E	P	I	F	D	K	320
TTG	GAA	GCT	GAG	CTA	GCC	AAA	ATG	ATT	TTA	TCT	ATT	CCA	CCC	GTG	AAA	1112
L	E	A	E	L	A	K	M	I	L	S	I	P	P	V	K	336

TO FIG. 12 (2)

TO FIG. 12 (1)

McLeod *et al.*

GGA	ATA	GAA	TTC	GGG	AGT	GGA	TTT	AAT	GGT	ACA	TAT	ATG	TTT	GGC	TCA	1160
G	I	E	F	G	S	G	F	N	G	T	Y	M	F	G	S	352
ATG	CAT	AAT	GAT	ATC	TTC	ATA	CCT	GTA	GAA	AAT	ATG	TCT	ACA	AAA	AAA	1200
M	H	N	D	I	F	I	P	V	E	N	M	S	T	K	K	360
GAA	AGT	GAT	TTA	TTA	TAT	GAT	GAT	AAA	GGT	GAA	TGT	AAA	AAT	ATG	TCT	1256
E	S	D	L	L	Y	D	D	K	G	E	C	K	N	M	S	384
TAT	CAT	TCA	ACG	ATT	CAA	AAT	AAT	GAG	GAT	CAA	ATA	TTA	AAT	TCA	ACT	1304
Y	H	S	T	I	Q	N	N	E	D	Q	I	L	N	S	T	400
AAA	GGA	TTT	ATG	CCT	CCT	AAA	AAT	GAC	AAG	AAT	TTT	AAT	AAT	ATT	GAT	1352
K	G	F	H	P	P	K	N	D	K	N	F	N	N	I	D	416
GAT	TAC	AAT	GTT	ACG	TTT	AAT	AAT	AAT	GAA	GAA	AAA	TTA	TTA	ATT	ACA	1400
D	Y	N	V	T	F	N	N	N	E	E	K	L	L	I	T	432
AAA	ACA	AAT	AAT	TGT	GGT	GGG	ATT	TTA	GCT	GGC	ATT	TCA	ACA	GGA	AAC	1448
K	T	N	N	C	G	G	I	L	A	G	I	S	T	G	N	448
AAT	ATT	GTT	TTT	AGA	TCA	GCA	ATC	AAA	CCT	GTA	TCA	TCA	ATA	CAA	ATA	1496
N	I	V	F	R	S	A	I	K	P	V	S	S	I	Q	I	464
GAA	AAA	GAA	ACA	AGT	GAT	TTT	TAT	GGA	AAT	ATG	TGT	AAC	TTG	AAA	GTT	1544
E	K	E	T	S	D	F	Y	G	N	M	C	N	L	K	V	480
CAA	GGG	AGA	CAT	GAT	AGC	TGT	ATT	TTA	CCA	AGA	TTA	CCA	CCC	ATT	ATT	1592
Q	G	R	H	D	S	C	I	L	P	R	L	P	P	I	I	496
GAA	GCA	TCT	TCT	TCA	ATG	GTT	ATA	GGA	GAT	TTA	ATA	TTA	CGA	CAA	ATA	1640
E	A	S	S	S	M	V	I	G	D	L	I	L	R	Q	I	512
TCA	AAG	TAT	GGA	GAT	AAA	AAG	TTG	CCA	ACA	TTG	TTT	AGG	AAT	ATG	TAA	1688
S	K	Y	G	D	K	K	L	P	T	L	F	R	N	M		527
CAT	AAT	GAT	TTT	GTA	ATC	CTC	AAT	TAA	AAT	GAA	AAA	TTA	TAA	AAT	ATA	1726
TAT	TTT	ATA	TAT	ATA	TAT	AAA	ATA	TAT	ATA	TAT	ATA	TAT	AAA	ATA	TAA	1784
ATA	TAT	GTA	TAA	TAA	TTC	AAT	TTG	CGC	AAT	CGA	TCA	AAA	TAC	ATT	TGC	1832
TCT	AC															1837

Fig. 12 (2)

FIG. 13 (1)

GAATTCTGCAGTTCTCTCGAATATATGGCTGCCCACTACCCGTAGGTATT 50
TGCACGACGACGCTTGCGTCACTCGGCGGCGTGACACACAACCTGCACTG 100
GCCGCCACTCGCGCGCATCCACGGTAGAGCTAACGAGTCTGCGATGGGGT 150
TAGAGACGCACACCTTTGACTCCCCGGGGCCTACGGAGACGACGCGGACGC 200
GTGTCTCCCCCTTTTCGCTCTTTTACTGTACGCTGGTAAAACGACTTTTC 250
GACGCAGCATGGTTCTCATCTTCTCGGTTTCACTTTTCTTTGAGTGCCTG 300
TGTGAGAGACGGTCGTCGCAACAAGAATCTCCTCCGCTCACGCCTTTCCCT 350
CACAGTCCTGTTTTTCCCTCCAGCTGTCACACATCCCGCTCGTTCCGCTGC 400
ATCTCCTCACATTTCTTGCAGTCAGATGTCTTCCTATGGAGCCGCTCTGC 450
GCATACACACTTTCGGTGAATCTCACGGCTCAGCCGTTGGGTGTATAATC 500
GACGGGCTGCCTCCTCGCTCCCTCTTTCTGTCTGAAGATGTTACGCCTCA 550
ATTAAATCGCAGAAGACCCGGCCAAAGGGCCTCTCTCGACGCAGCGGAGAG 600
AGAAAGATCGAGTCAACATACTCTCCGGTGTGAAGACGGATATACACTC 650
GGTGAGGGAAGAACTACAGACGTCACGTGCCTGTGCCAGCACATAACTG 700
CAGATTTCATATATATATATACATATACAGATGTGTATTTTGTGTGTATAG 750
TTAAGCAGAGGATGGTATTGAAAATGGCTGTGGGTGTATTCTTATTCGCC 800
CTGTGGCGCTTTTGGAGAAGGCCCTGGGGAAACGGAAGCCCTGGCACAAG 850
GGCTGCCGGCTAAGCTTCAGAAACCGCAGTTAATAGCTCGAAAGTACCGT 900
ATCCAAACGTTCTCTTTTATCCACACAGTGTGTTGGACACAAGCGAAGCC 950
GAAAAGTGTCTTGCACGTGGCGAGTTTTTCGGTGACAAAACACACGCGCCA 1000
CTCCGTAGAAATACCGGATCCGAGTTTACCTGCTGCAGGCTTCGGAACGC 1050
TGCTTTGTTCCGAAGATGGCCTCGTGGTTTCGATGGGAAATTGGAGGGTG 1100
CAAAAGTGCCCGGCGCTCGTGGCCTGCGCCATCTGGCATCGTGGACTGGC 1150
CGTCTACCGTGATCCTCGCGTCCCTTCCAAAAAATCATTTTTCTCTGCTT 1200
CGCCTTCTCGTTTCGTGTCACCGGGATCCGTCTGCAGGTACTCCCCTGGCG 1250
ATGCTCGTCTGGAATGAAGACCGGCGGGCCCCAGGACTACCACGCCCTCGC 1300
GACAGTCCCGCGTCCAGGTCACGGGGATTTACCTACCATGCAAAGTACC 1350
ACATTCACGCGAAAAGCGGGGGCGGTCTGGAGCAGCGCGCGGGAGACTTTG 1400
GCGCGCGTCCCGCTGGAGCAGTCTGTTGAGAAGTGGCTAGGCATGCACTA 1450
CGGCACCAGCTTCACAGCTTGGGTCTGTTCAGGTGAGACGAAGCCCAGAAG 1500
GTTTACAGCAGAGTGGATGAAAAGACAGAGATAGACAGGTCTTTCGCTGGAG 1550
GCAGTACGCGGATGGAAGACAACGTTACGGCGCTTCCGATTCATGGGGC 1600
AAGCGTGGCTAAATTTTCCATGACTCGACAGCGGTGACCCTAGGATCGCGT 1650
CGGTTTTGTATGCCTGGTTCTCTCACGCCCTTAGGTTGGTGATGTCCTCTGT 1700
GCCCCGATCGCTCCGAAGAAAGTGGGAGCGGCAGCCGCCAACTCGCCAAG 1750
ACGTCGATCGCCTTGGCGTGGTCCGCGTGAGCCCAGATGGAACCACATTTT 1800
CTCGACGCGAACAACCGCCTTTACGACGAGCGAGGAGAGGAACCTCGTCCA 1850
GGAGGAAGACAAAGCCAGGCGTCGGCTTCTTTTCGGAGTCGACAACCCGA 1900
CGCCAGGAGAAACAGTGATTGAGACCAGGTGCCCGTGCCCCCTCCACAGCT 1950

FROM FIG. 13 (1)

FIG. 13 (2)

GTTTCGCATGGCTGTGAAAATCAACCAGGTGAGGTGGAGCAGTGCGATGAG 2000
CCATCTGTTCACTGGATCCGTAAACGCGAAGGTCATCCGTGGGGGAAAAA 2050
AGTGAATCTACGGAAGGTGAGCTGGCTTTGGCCGTGACACGTCTAGTCTA 2100
CCCTGCAGACCTACCATTTGGCGAATAGCAAAGCAGCGGGGGAAGGCGTC 2150
ACCCGGAGAAGGGTGTGCGAGCAGTGCGCCACCCAGAGGCTCGGAAGACC 2200
TCCGCGAACGTTGATGGTGTGCACGGTGCGGTACCTTTCAGCGGCGAAAC 2250
CCTCCATCCGAGTGTGCAGACAAGTCATCACCCAGTTGTATGAAGCACC 2300
CTGCCTTCGATGGTGTCCCTACTTTATCCTCTCAGACCCGATCTCTGGGC 2350
GATTCGATTGGCGGATGCATCTCCGGTGCAATCGTGCGGCCACCGCTGGG 2400
CCTCGGTAAAGCAGTCTCGTTTTCTGTGTTCCTCGGCTCCTATACAGCAC 2450
CTGACCACGTTTCTAGGTGGTGTGGCGACAGGTCGGACCTATATTCGAGA 2500
CGTGACACAGTTCGTCCAAATTGCTCGTTCATGCACCAGCATCTCCTTGC 2550
CAGACACCCACACACCGCATAGGTTTGCTTGACAAATGAAACTGACAAA 2600
TACGACCTGCGGGGACTTGTGACAACGTTGCCCTTTTGCCGTTTTCTTGC 2650
GAGGTCGTGACTGAGGCGCTGGTGAAGAGCGAGACTGGGCCGAGGCGTGT 2700
GTTTCCATGCAAACAGAAAGCAGGCTGATAGAGACAATGCAAACGAGCGGA 2750
CGTGGAAGCGCAGTGCTGAATGCATGAACATAAAGGTGCACACACCT 2800
GCGCACCAACCCGAGATGCAGCGACCGACGGCACACCTCTGTGAGGTGCAG 2850
ATGACTCTGCATCAAGAATCAGTGCCTCAGAGACCCTTTTCCCCGTGTAG 2900
TTTCTCAGTGCGGCAGAAAGAGTTTTTCGTTGCTCTGTTTCAGTCCATCCAC 2950
CACCAGCAGTTGGCGCCAACTGCGAGACCGAGAAGGCAGCATGCGAGAAT 3000
TCAGAGAGTGCAAGGGAGAGTTTTTTGAATCATGTTTTCTCTGATTTCTT 3050
GCTGGAGGTCTGTGCATGTAGGCGAGCCGTGTTTCGACAAAGTGGAGGCG 3100
GAGCTGGCGAAGGCGATGATGTCGCTCCCTGCTACGAAAGGGTTTGAGGT 3150
ATGTGTGCAACTTTCTCCAGAGAGGTGATAATTGAGCACGACGCATGCAA 3200
TTTGTGGTCAGGCCCAATATGTACAGCTCAGTTTCCACCGAAGAAATCAA 3250
CACTGGTCGGGTCTTTTTCAGCCACCTGTGGCCGTGTCGCTTTCACCTCTT 3300
GCCTGGGATAGATGTGAGGCACACTTCGTCAACACCTTGCCGCTGGCTCT 3350
ATATCGGACGCCACCCTGAAATCGCGTTGCGAATGTTTTCTTTTGCATTTCC 3400
TGATGCATCCGTCTGTGTGTGACAGATTGGCCAGGGCTTTTGCGAGTGTAC 3450
GTTGCGAGGCAGCGAGCACAAACGACCGCTTCATTCCCTTCGAGAGAGCGT 3500
CGTGTTTATTCTCGGAATCAGCCGCGAGCACGATCAAGCATGAAAGAGAT 3550
GGGTGTTACGCTGCTACACTCTCACGGGAGCGAGCGAGTGACGGTAGAAC 3600
AACTTCTCGACATGAAGAGGAGGTGGAAGGGGGCGGGAGCGCATACAGC 3650
CGGATACCCTCCATGTTACTGGTGTAGATCAGCAAAACGGCAACTCCGAA 3700
GATTCAGTTCGATACACTTCCAAATCAGAGGCGTCCATCACAAGGCTGTC 3750
GGGAAATGCTGCCTCTGGAGGTGCTCCAGTCTGCCGCATTCCACTAGGCG 3800
AGGGAGTACGGATCAGGTGTGGAAGCAACAACGCTGGTGGAACGCTCGCA 3850
GGCATTACATCAGGTGGGTCCCGACCCGTTACTCGCGCTCCGCTTCTCTCT 3900

FIG. 13(3)

CCAGTTCGGCGTTCGACAGCACTCGTTCAAAGTG GTTGGT TTTCTGGCC 3950
 AGTGGCAGCATTGGCTGTAAAGAACACACTGTTGCTGGCTGCTTTCAATA 4000
 GGTGTAAAAAACTGGTGTCTTTTCATTTCAGTCTACAGCTCTGATGCAC 4050
 CTTTCTGGTGCCACGTCAGTCCCTTGCTGCGGCCATCGACTCAGATAGAA 4100
 CAAGATCCCCCAGATACAAGAGAAATGTCTTGAGCCAAGAAGACGGCTGT 4150
 CTAATTACACGATACGGACATCAGTAATGAGATTTTAACAGAGGGGCTTC 4200
 CAGCATCGCTGCAGGATGTCGCGTCGCGACCTCAGGTTGTTGATTCTGTG 4250
 CTGAGAGACACACATTGTGCAACTGCTGCCTGCCCTGTCTTGTTCGTGCG 4300
 TCCGTGGTGAAGTACCATCGACGTGATGAACAGCCTGAATGCAGACGTGC 4350
 TCTAACGGGGTGCGCACCAACCCCAAGAGGACGGTGTGACTACGTCCGTGG 4400
 CGTGGAATTGATGTGTGTTTCATCAGGAGAGAACATTTTTTTTCGGGTGGCC 4450
 TTCAAGCCTGTTTCTTCCATCGGCTTGGAACAAGAACTGCAGACTTTGC 4500
 TGGTGAAATGAACCAGCTAGCTGTGAAAGGTAAGAGGCATTTGCTTATTT 4550
 GGGTCTCGACTTAGGCGGTTCACATTTCCATTCACTCTTATCAACATTTGC 4600
 AAGGTCGAAATCTGTGGTGCACATGGATGCAGTCGAGGCGGGTCACTCA 4650
 CATTCGATTTTCTCCACACGCTCGCCCAACAAGAACTGGTTTGGTGTTC 4700
 TCGTGAATTCTGTTGACAGGCCGCCACGATCCCTGCGTCCCTCCGCGAGCC 4750
 CCTCCTCTGGTTGAGAGCATGGCTGCCCTTGTAAGCCGGCAACATAATCT 4800
 GGGAAAACGAAAACGATTGCCAGAGCGGGGATGGGCACAACACGGATCCG 4850
 TGATGTTCCGTAGTACCTCGAGTCTCTCTGAGTCTTGTGCGGGATTGGTG 4900
 ACTGCACCCAAAATGTGTTGGAATCGAACGCTGGATCAGTGAACCTCCTTG 4950
 GCTGATGTCTCTCAACCGTATGACTGCTTCTCAAACAGCTCATATAACAC 5000
 CCGTGCGGAAGTGTAGCAACAATTTTCCTTCACAATTTGGCCCCGGGTCCGT 5050
 GCAAAGACATTATGCAAAGCAGCCCTCAGTCGTGTGCCTCGCTTGCCTGC 5100
 AGTTTCACGTAAGACTGGCATGAGGACCGAACTACCGTGCAGGGAAACAT 5150
 GCTGACGTCCCCCGTAGAATGTTCTTGAGGGAACTCGCGGTGTGGCCTCC 5200
 TTTCCTCGAACAGTAGGACAATCCTGTCTTCTTGTGCTTGTAGATCCTTG 5250
 CCGTTTCATTAAACCCCTCTTTGAATTTCGTCACTTGCCTCGATGACATGTC 5300
 CCTTAGGTGATTGGCGATCTGTGCCTCCGCCAGCGCGCCCGGGAAGGGCC 5350
 GCACCCCTTTCTCGTCCCTTCTCAACACAGTGGTTGCCCATTCTTGCCTGAC 5400
 CTCTACCTTGTTCCAAAAACCTTGTGCATACGGGGTACACCAGGTTCCTCA 5450
 CAAGGAGAATCGTGAGGCGGTGACTGGCCAGCGCCACAGATTGCTGTTCA 5500
 TGCACAAGAAAGAAAACAGCGCATTTCCGCCACAACCCAGCTGCATGAAG 5550
 TTGCTGGATATCGTTCCGGCGGTGCTCGGCCTTCTTCTCTACGCTCGCGA 5600
 TGATACGTGCGGAGCTTCATCAAGCTCCTTTTGCAATTGTTAGTGGCTCCC 5650
 AACAGAACCCTTTGTGGAAGGGAATCTGGTCTCACGCTTGCAGGAGAGAG 5700
 TTCCGCTTTGTTACGAAATAACGAAGCCAAGCAGCTCAGTTGCATTCAG 5750
 CCTGCACACAGTTGCATTACGCCTGCACACTAAACACGGGCGAAATCGTTC 5800
 GCGTGATATGTAGTTCTTCGGTTGTACGGTGATTGTGCTCGTGTTCGAA 5850

FROM FIG. 13 (3)

FIG. 13 (4)

CAACTAAACGTTTCTAATGCTGGATCCGAATTC

5883

FIG. 14A

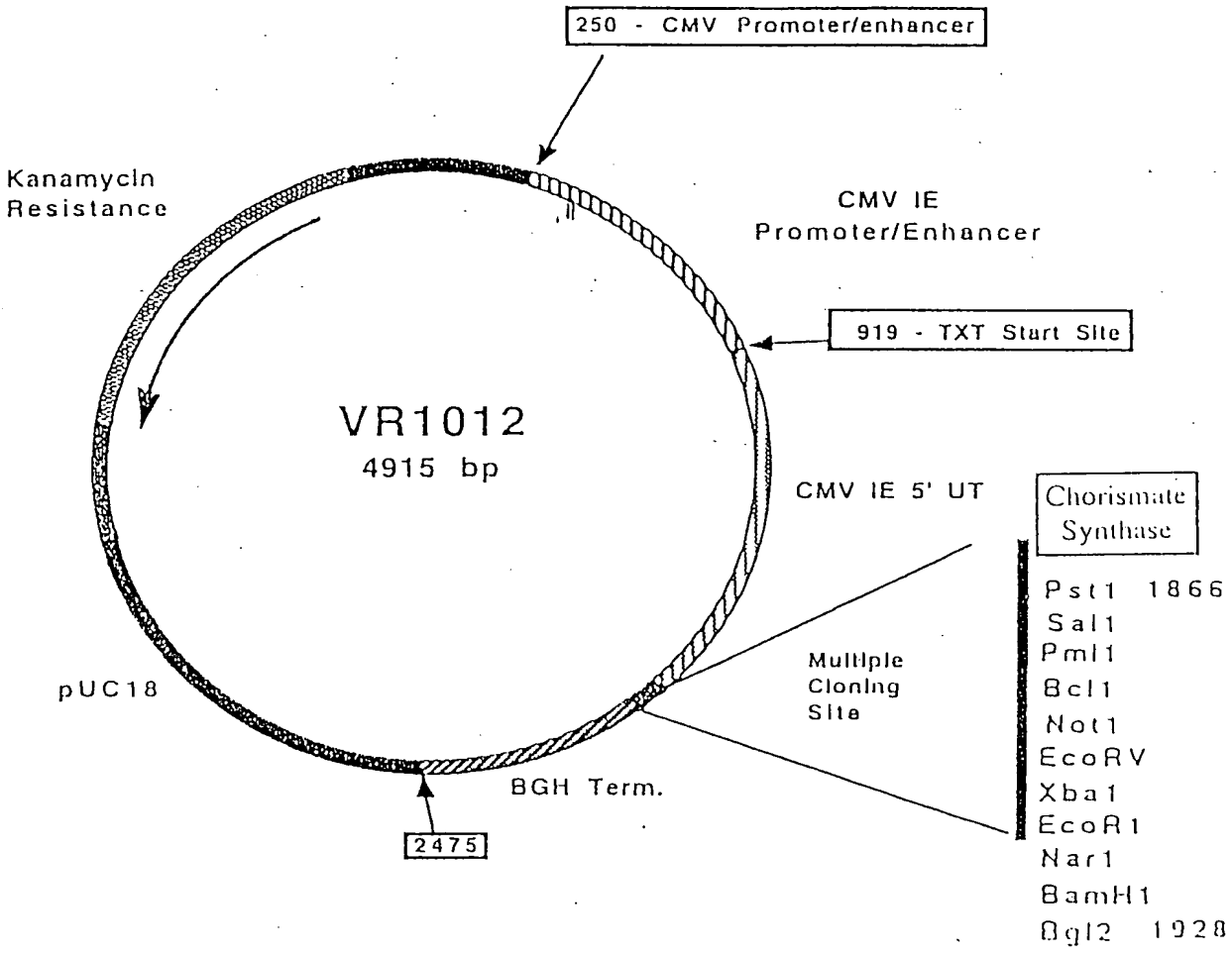
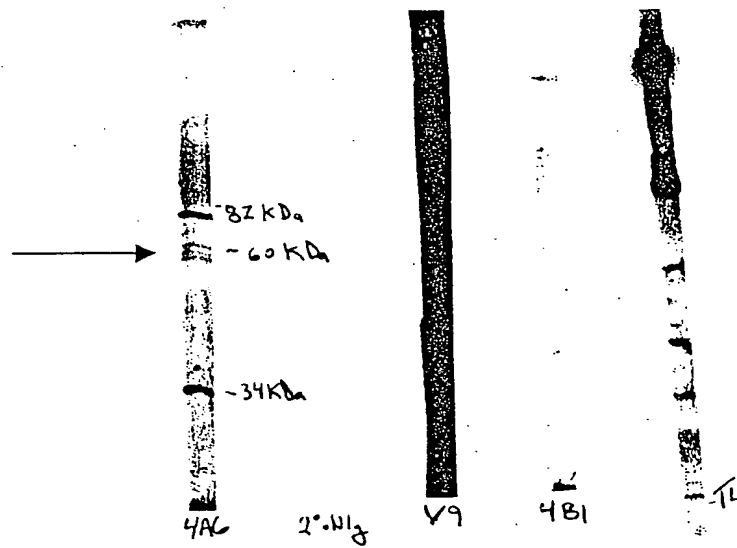


FIG. 14B



Key: —————> Indicates Chorismate Synthase

FIG 15

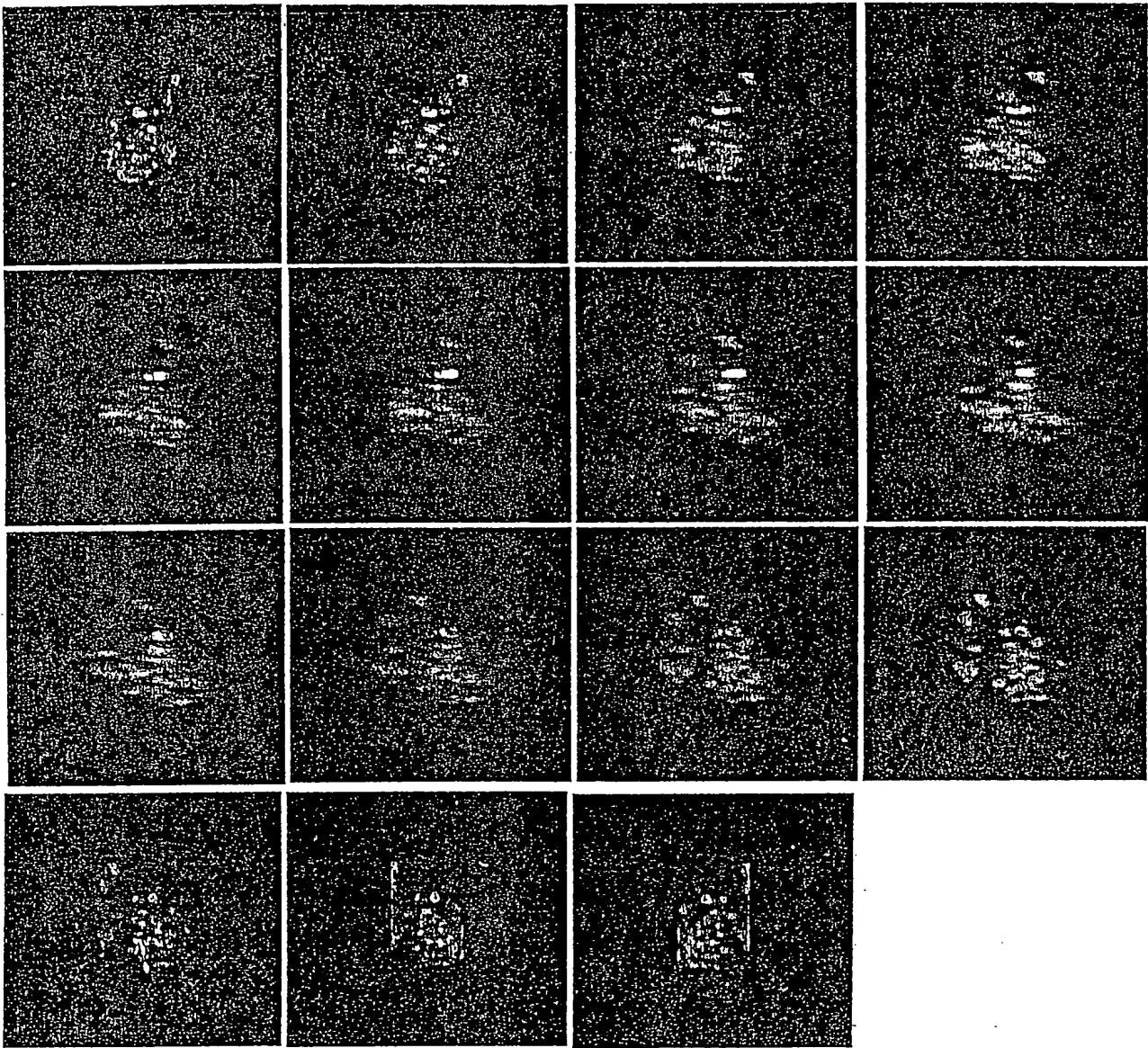


FIG 16A1

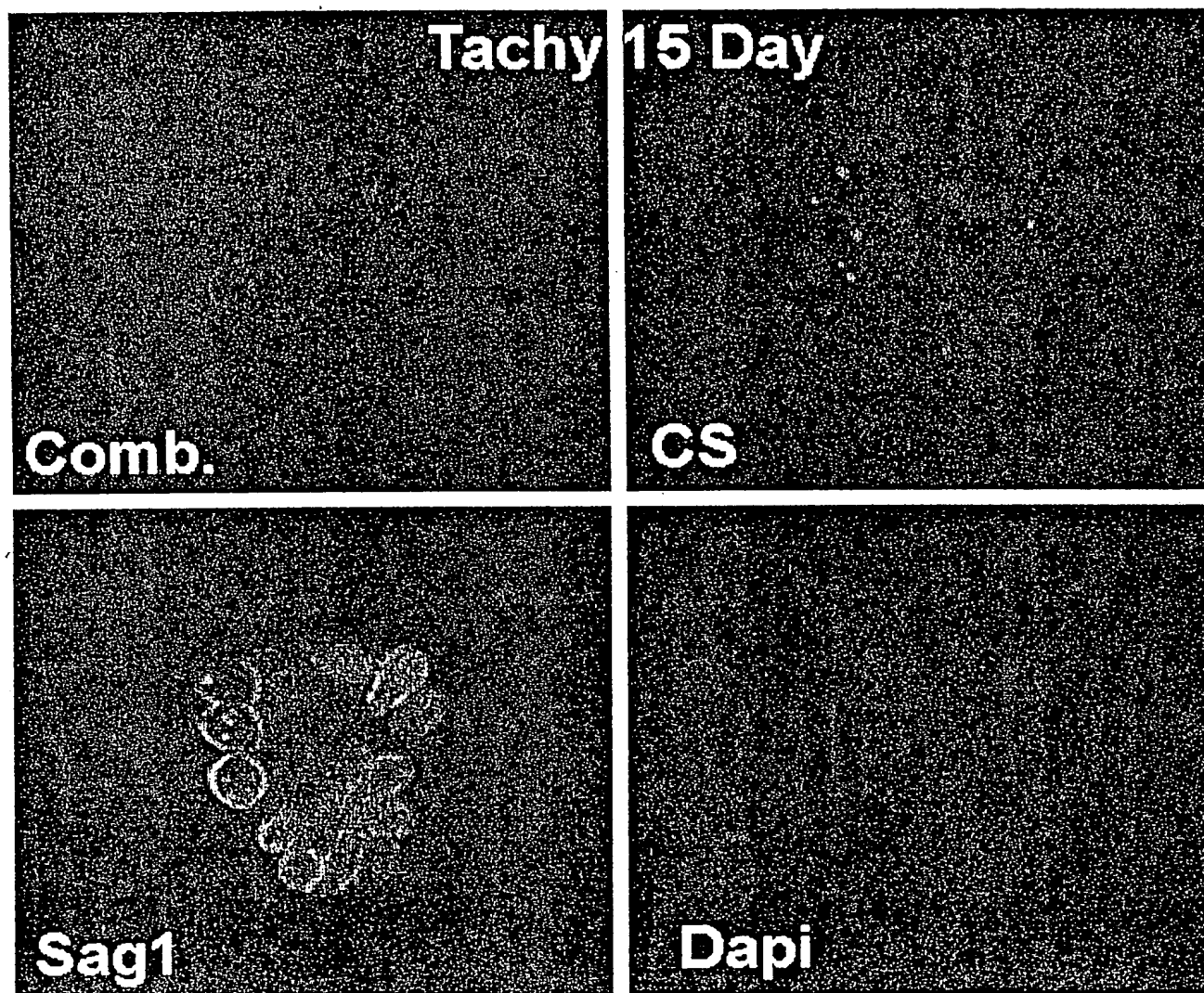


FIG 16A2

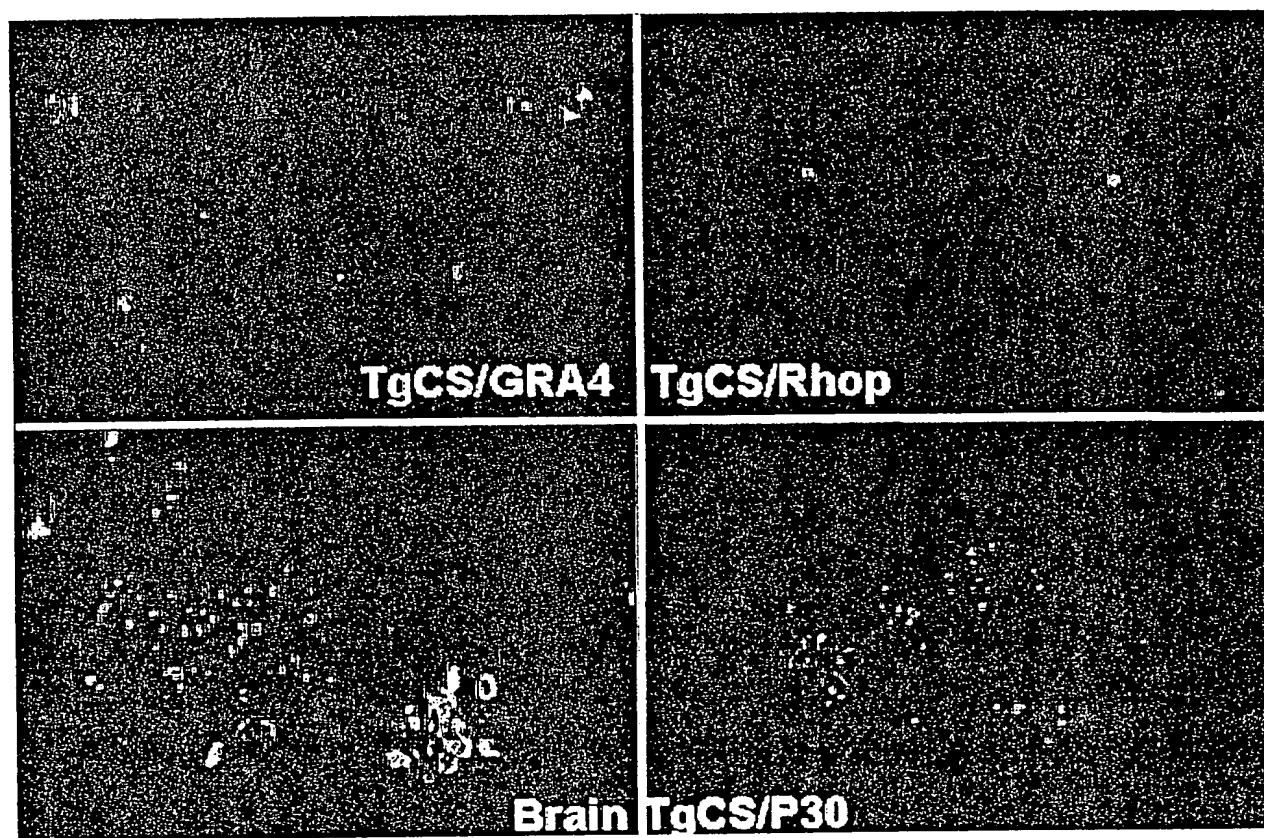


FIG 16A3

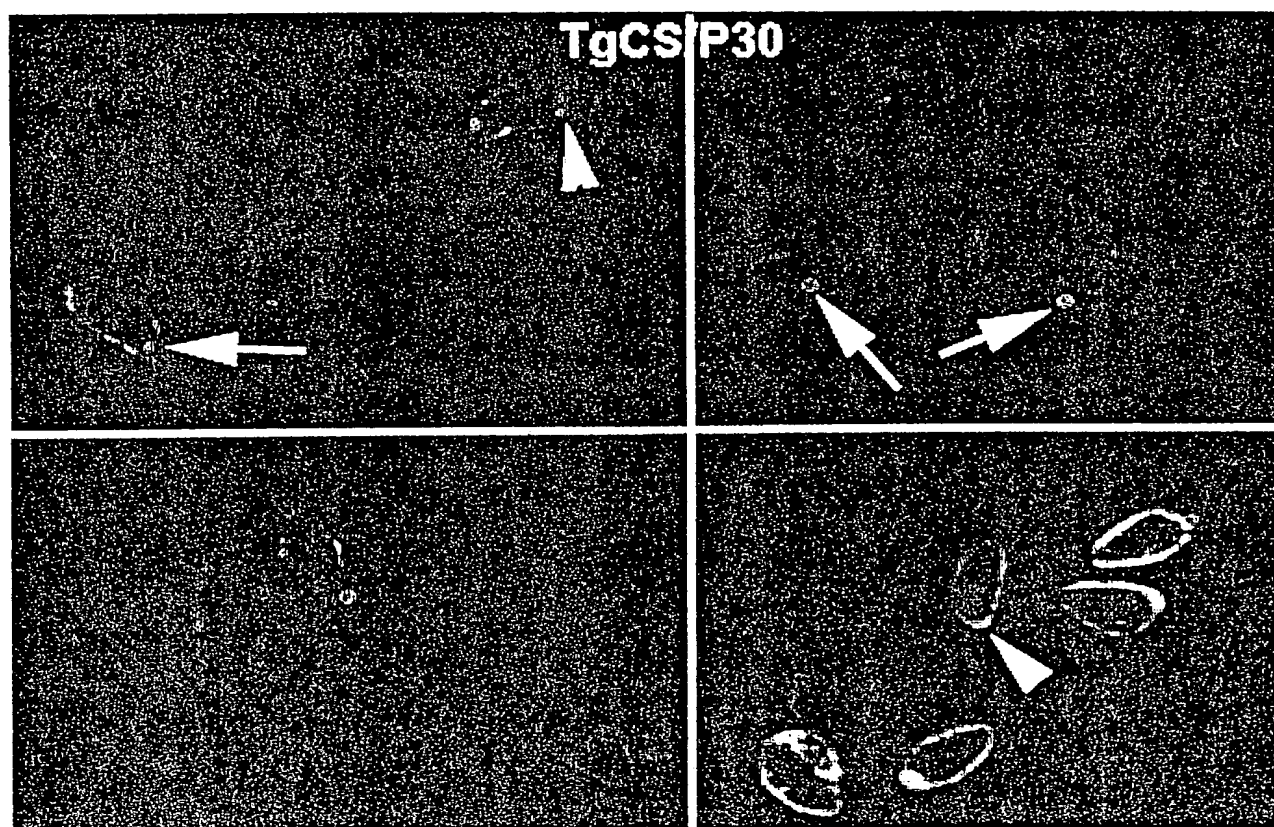


FIG 16B1

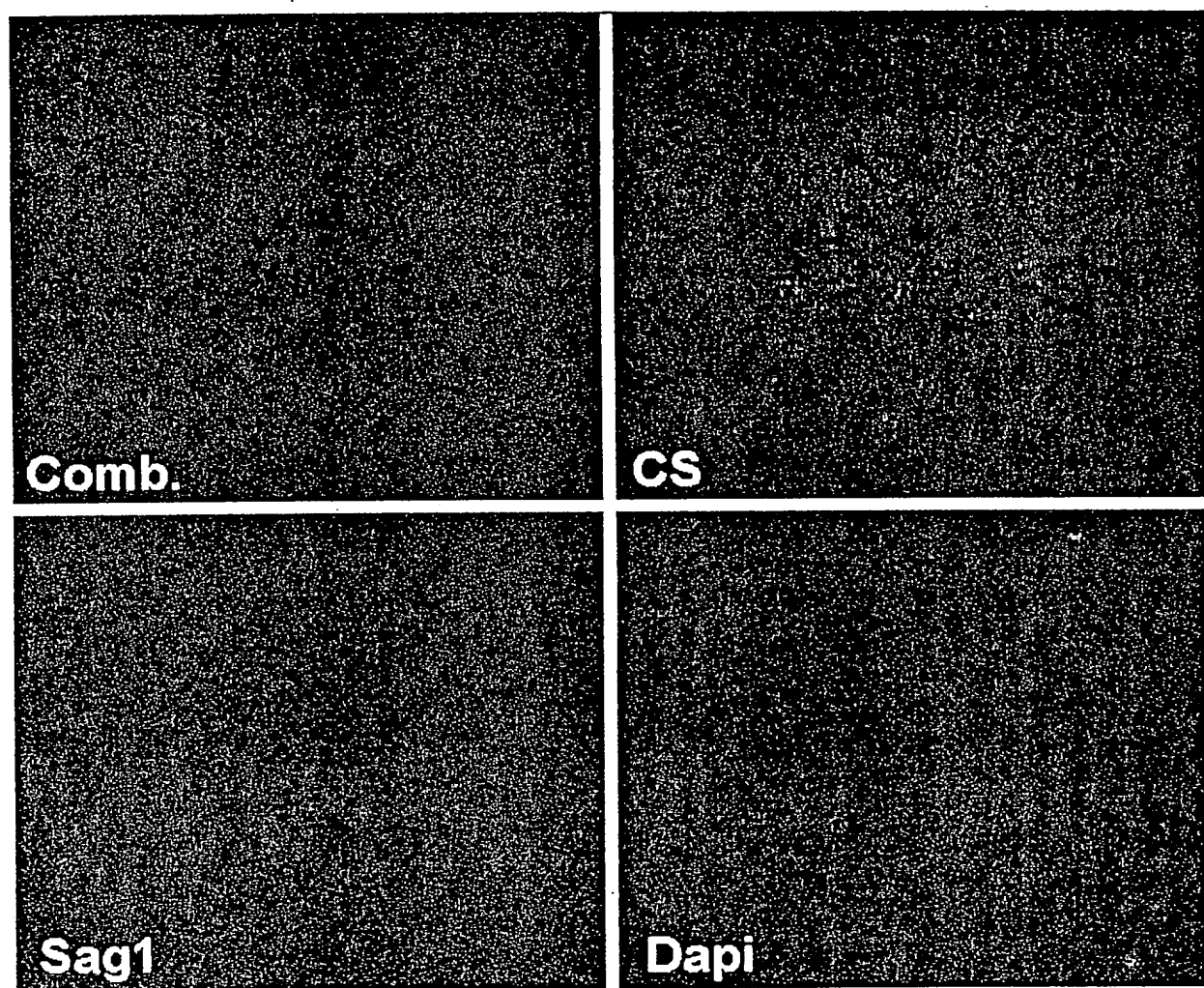


FIG 16B2

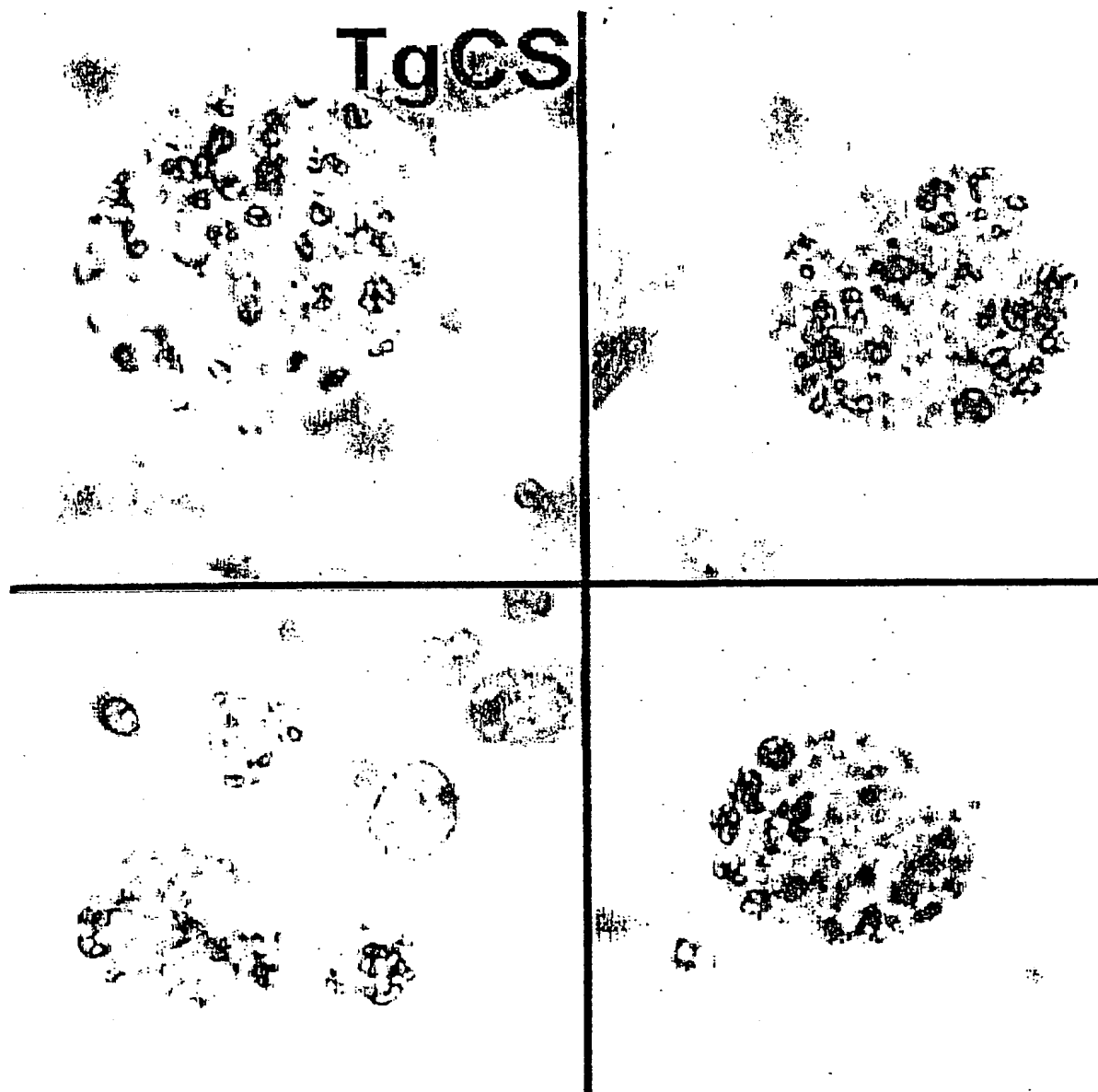


FIG 16C

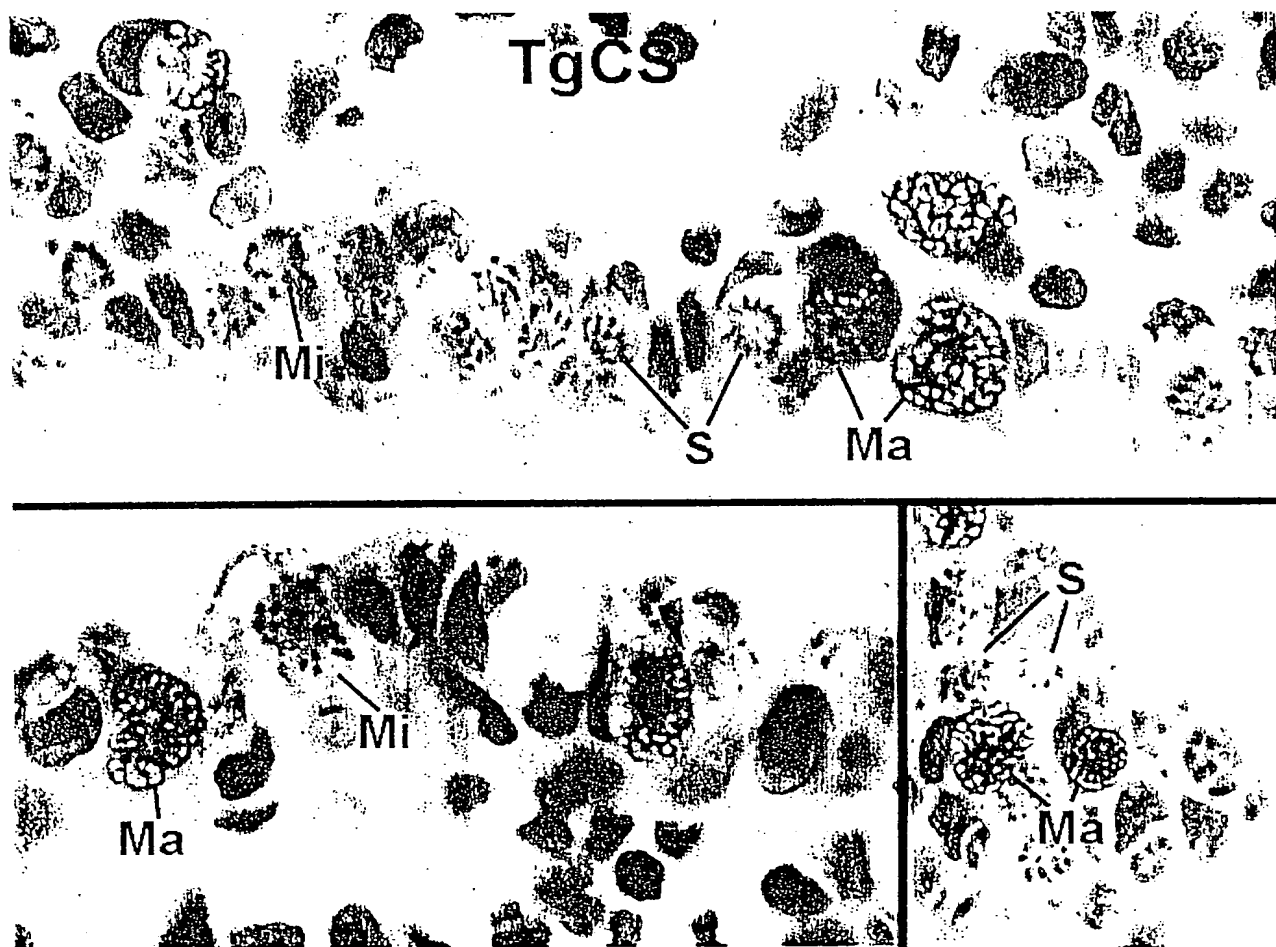


FIG. 16D

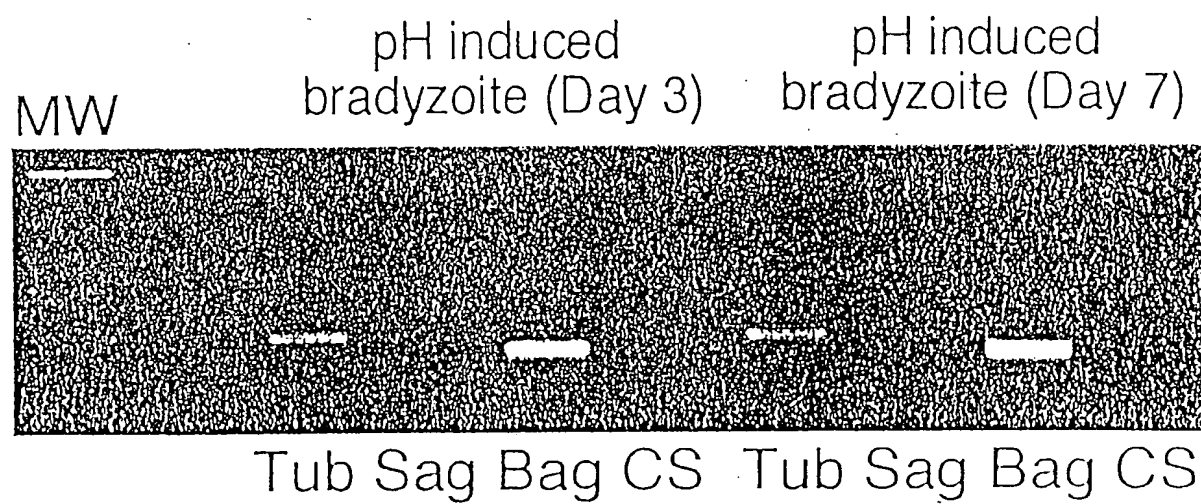
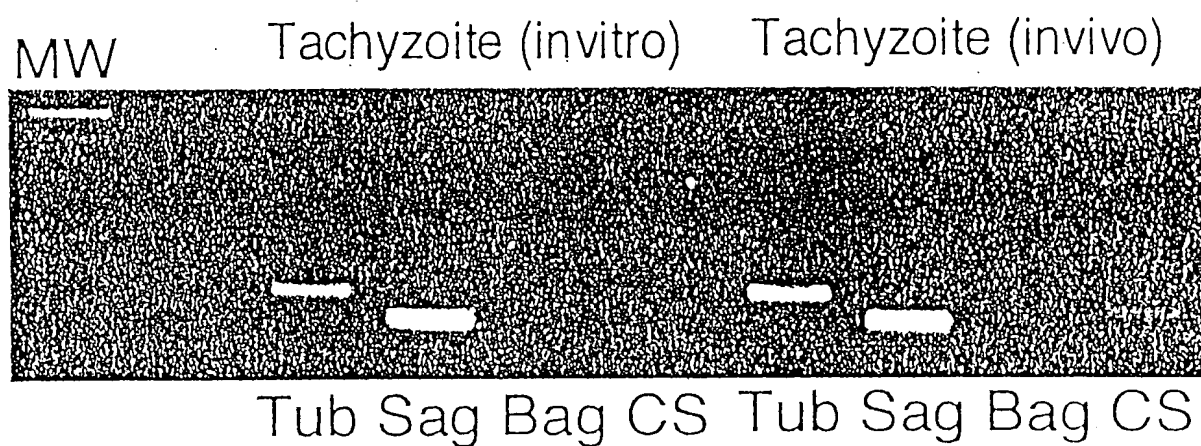


FIG. 17A

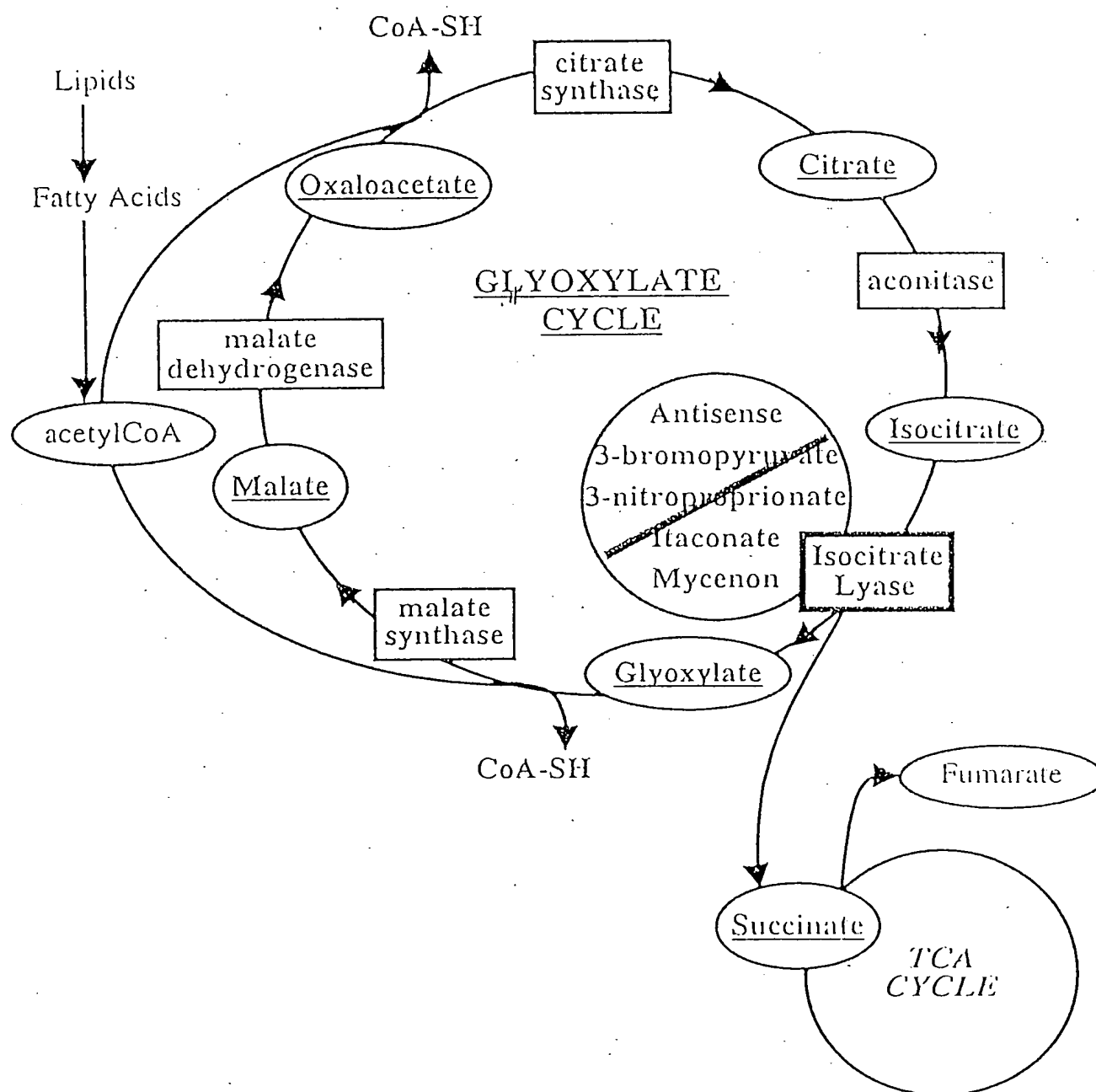


FIG. 17B

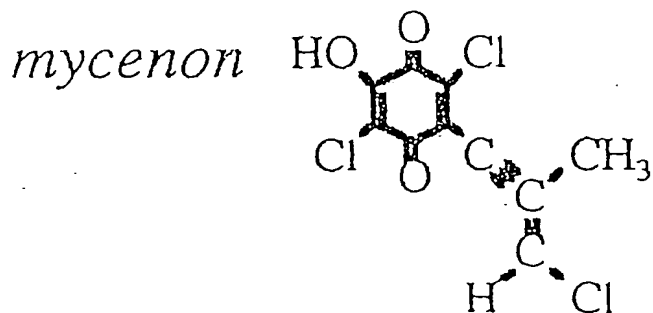
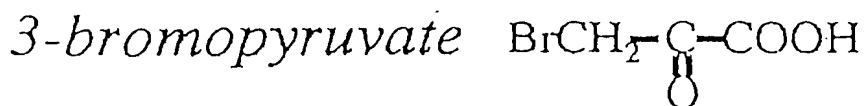
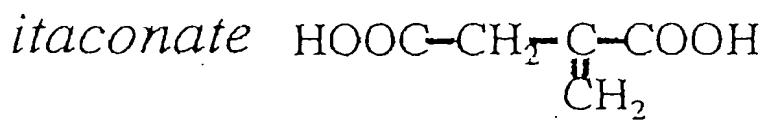
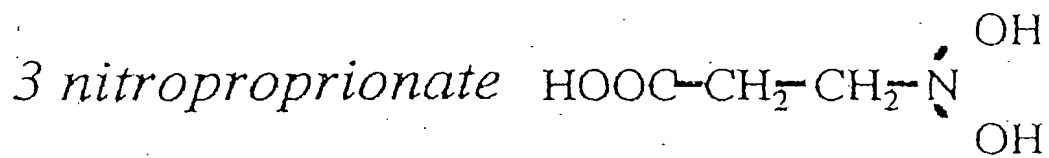
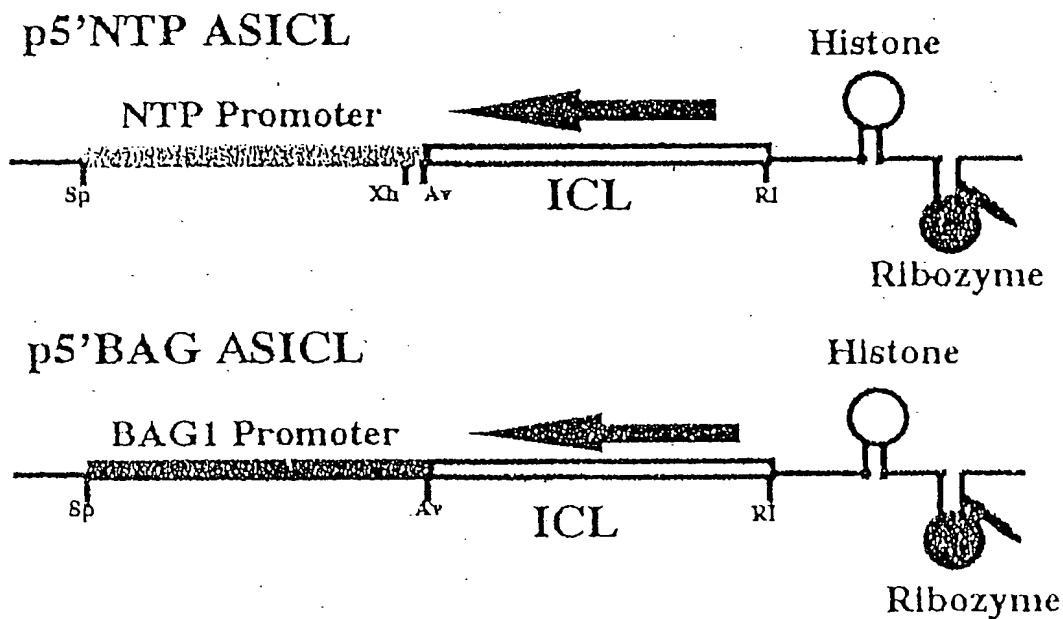


FIG. 17C

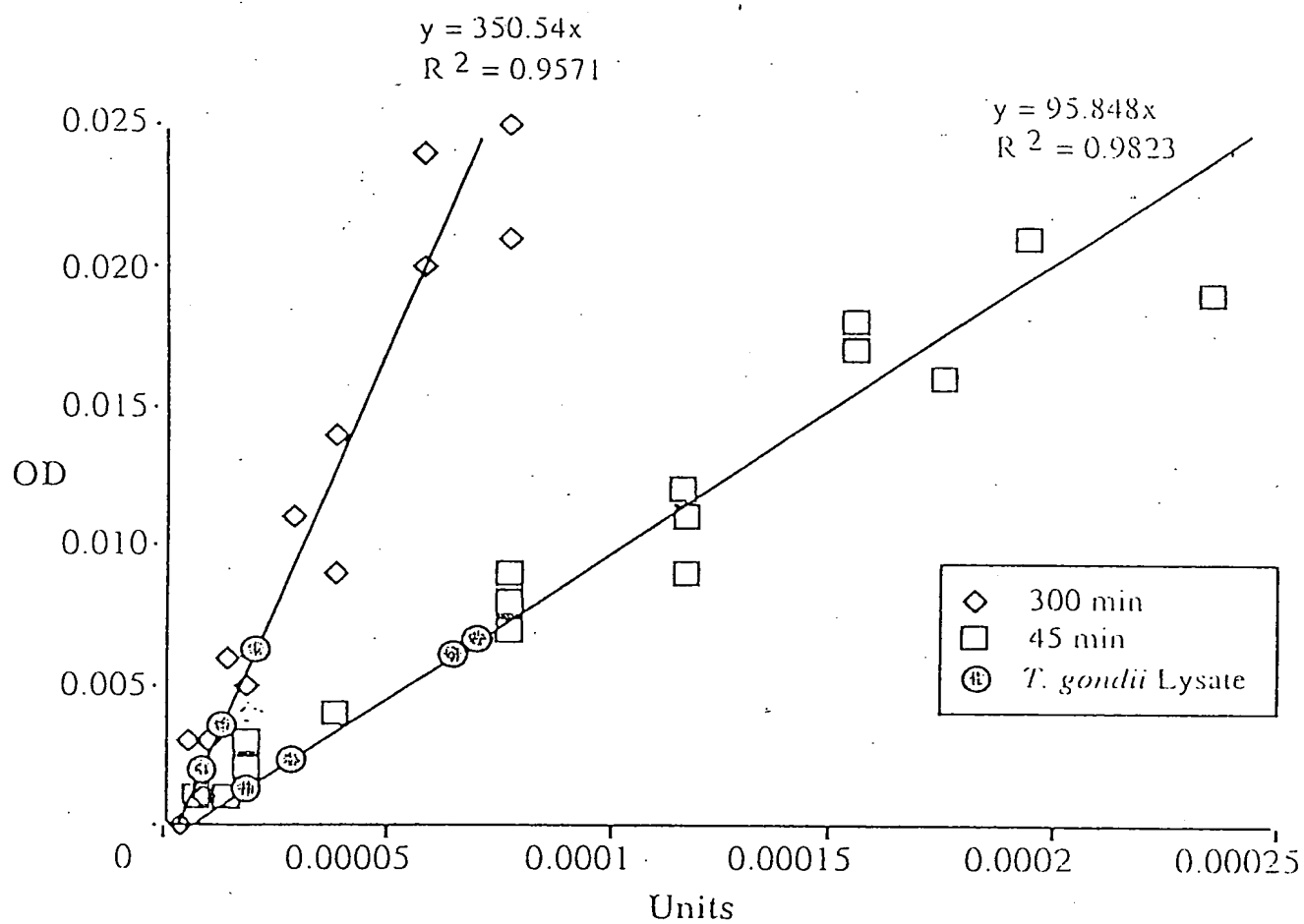
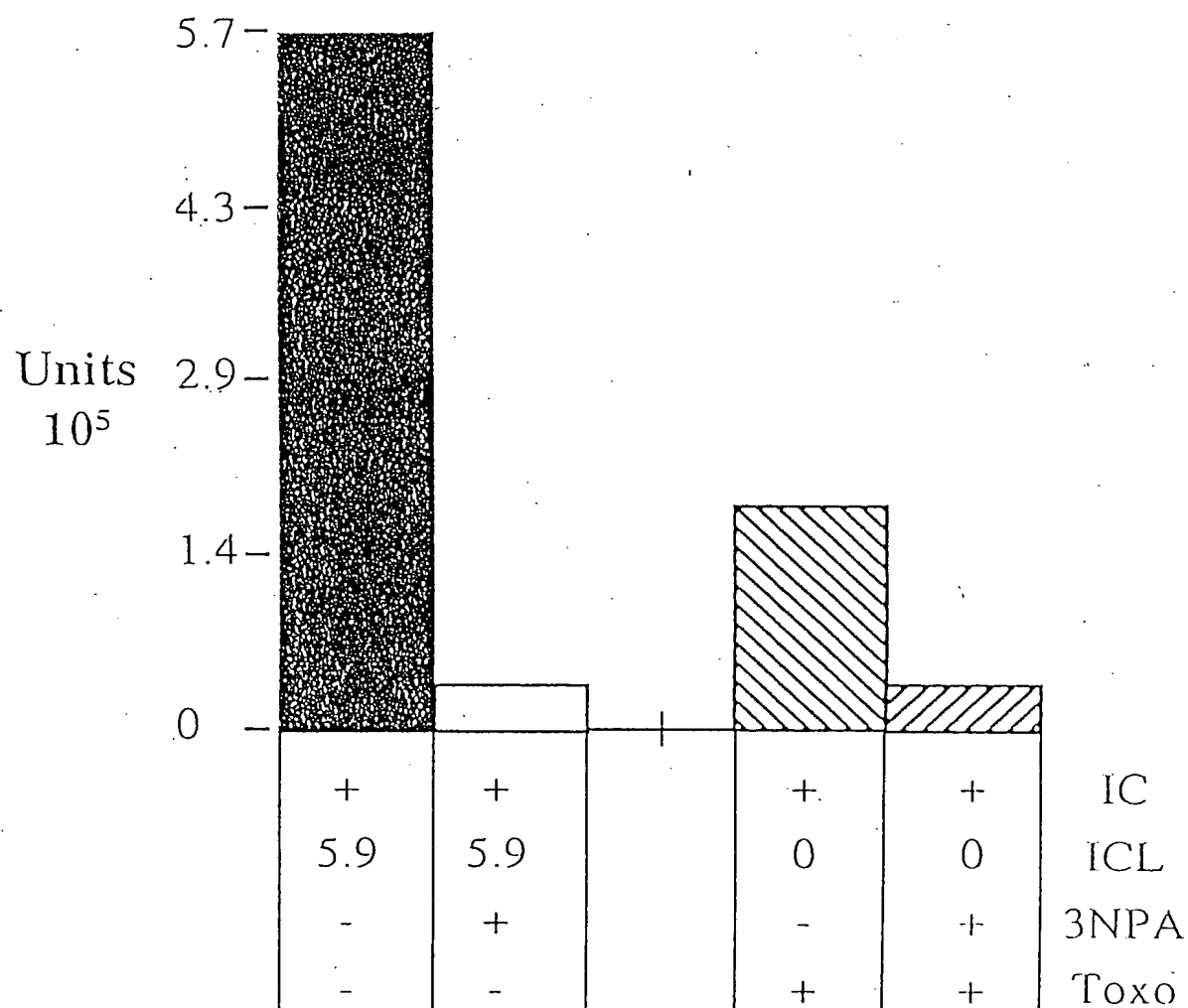


FIG. 17D



IC = Isocitrate [4mM]

ICL = Isocitrate Lyase [10^{-5} units]

3NPA = 3-nitropropionate [$1\mu\text{M}$]

Toxo = *T. gondii* Lysate

FIG. 17E

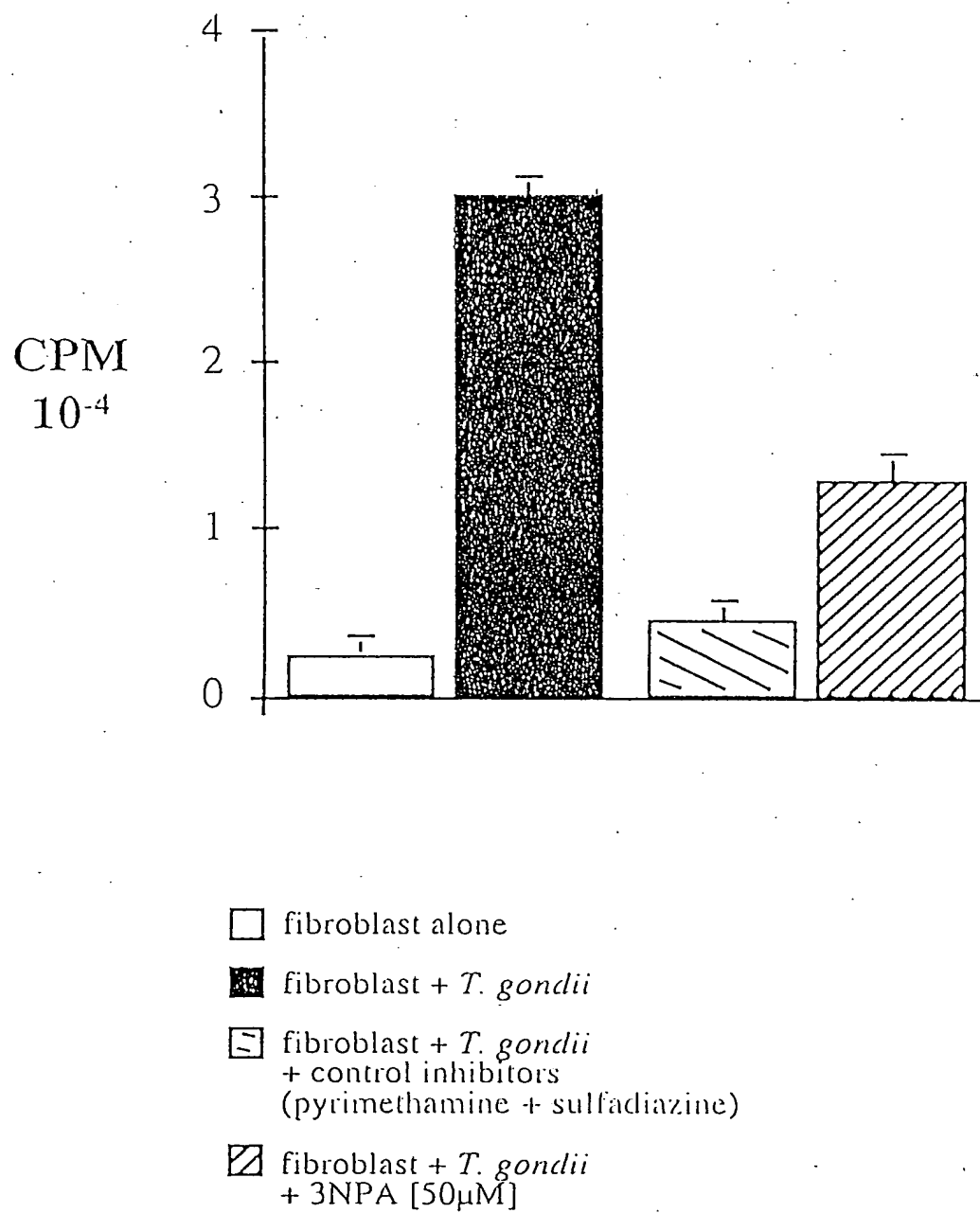


FIG. 18

AATACCCCTCCGAGTTCTATACGTTTCTTCGGTTTTTTGCTAAGCCACAAAC 50
 TGCAGGCTTAGCAGGCCACCTTCCGTCGTGAACCTCGTTCGCCGAGTTTACC 100
 GGCCTCACACCTATTTTCGTTGCCGTTCTGGAAAGTCAGTAAGGGACCAC 150
 CTTACGTCGAGTTGACCGGTCTGCAATGACCATTGAGTTTCGATGTCCTCG 200
 AAATCCTTTTGTTTTGATTTCCGCAAGGAGTGTCTTGAACCAC'TGTCGGT' 250
 GTCTACTTCCTTTTTTCGTCGCGCTTCCGCGCCGTCTCCCCGTCTTCGTCT 300
 CCGCCTTCCGTCTCACAAC'TTCCCTTCA'TTCTCACAGCATGGCGTC'TCGT' 350
 GCTCCCCATGCTGGACAGCGCTTGCGCAGCCTCATGCAGAAGAAATGCGT' 400
 CATGCTTCCTGGGGCTTACAACGGTCTCACCGCGCGCCTCGCGGCTGAAG 450
 CAGGATTTGAAGGAGTCTACGTCTCTGGAGCTGCTCTCAGTGCATGCCAA 500
 GCGTCCCCGATATCGGCATATTAGGTCTCGAAGACTTTACTCGAGTAA'T 550
 CTCCCAAGCCGCCTCTGTCAACAGCCTCCCTGTTCTCGCCGATGCAGACA 600
 CGGGGTTCGGTGGCCCTGAAATGGTTTCGGCGCACTGTCTTCGCGTACAAC 650
 CAGGCGGGCGCGGCTGGGCTGCACATTGAGGACCAGCGTTTGCCGAAGAA 700
 GTGCGGGCATTTGGAGGGGAAGCAGTTGGTGTCCATTGAAGAGATGGAGG 750
 AGAAAAATCAAAGCGGCCGCTGCGGCGTCCCAGGACTGCTCGAACGGCCGAC 800
 TTCATCATCTGCGCTCGCACGGACGCCCGCAGTGTGACGGGGCTTGATGC 850
 GGCTGTGGAGCGAGCAGTCCGATACACGGCAGCCGGAGCAGACATGCTT'T 900
 TCCCCGAAGGACTGGAGACAGAGGTGAGAGGTGGAAAGAAGAATCAGAGG 950
 AAGAAGGCGTCTGTATTGGAGAGGCAGCGAGAGGCAGTCCCTCTTGGAAGA 1000
 GTTTCAAGCATTTGCGCATGCATTGGCGGTTTTTGCTTGCAAAGCGCCTT' 1050
 TCGGGGGGGCCCTATCTGCTCGCAAATATGACGGAATTTGGAAAGACGCCC 1100
 ATCATGGAGCTTTCCACCTTCGAAGGCCTTGGATACCACTGCGTTATCTA 1150
 CCCTGTTTTACCTCTCAGAGTCGCCATGAAAAGCGTCAAGGGCATGCTGC 1200
 TCGACTTACGCAAGAA'TGGCAGCGTTGGCCATAGCCTGGAGAAAA'TGTAT' 1250
 ACACGGCAGGAGCTTTATTCCACTCTGCACTATCGGCCGGAAGGGACGTC 1300
 GACGTATCCC'TCAGCGAGTGTGTGCATGGACAAAGCCGTGGAAGATACCG 1350
 AGGCCTAGGGAGTCTCAGGCTCGGCATTTTCTTTTCTCGACTGGTCTCA 1400
 CCAATACAAAAGACAATGCTCACAGACGAAAAGCAGAAGTTC'TGAT'GTA 1450
 TTTATGAAACG'TGAAAAA'AAAAAAAAAAAC'TCGAGGGGGCGGCCGCTA 1499

FIG. 19

YPPSSIRFFGFC*ATNCRLSRPPSVVNSFAELPASHLFSLPFWKVSKEPP 50
SRAVDRSAMTIEFDVPKSFCFDFRKECLEPLSVSTSFFVALPRRLPVLVS 100
AFRLTTSLSHSHSMASRAPHAGQRLRSLMQKKCVMLPGAYNGLTARLAAEA 150
GFEGVYVSGAALSACQGVDPDIGILGLEDFTRVISQAASVTSLPVLADADT 200
GFGCPENVRRITVFAYNQACAAGLHIEDQRLPKKCGHLEGKQLVSTIEEMEE 250
KIKAAAAASQDCSNGDFIICARTDARSVDGLDAAVERAVRYTAAGADMLE 300
PEGLETEVRGGKKNQRKKASVLERQREAVALEEFQAFahalAVLPGKAPF 350
GGPYLLANMTEFGKTPIMELSTFEGLGyHCVIYPVSPLRVAMKSVKGMLV 400
DLRKNGSVGHSLEKMYTRQELYSTLHYRPEGTWTYPSASVCMDKAVEDTE 450
A*GVSGSAFSFSRLVSPIQKTMltDEKQKF*LYL*NvKKKKKNSRGGPV 499

FIG. 20A (1)

		10	20	30	
B._napus	1:	MAASFSVP	SMIME	egRFEAEVAVQ	TW: 28
A._thalian	1:	MIDKP	NQIME	egRFEAEVAVQ	TW: 25
R._communi	1:	MAASFSGP	SMIME	egRFEAEVAVQ	AW: 28
castor_bea	1:	MAASFSGP	SMIME	egRFEAEVAVQ	AW: 28
G._max	1:			EAEVAVQ	AW: 10
Cucurbita	1:	MATSFSVP	SMIME	egRFEAEVAVQ	AW: 28
P._taeda	1:	MAIYSAQA	ENSILE	egRFEAEVAVQ	AW: 29
N._crassa	1:	MAANNMVNPA	VDPAL	DELFAKEVE	VKKW: 30
C._cinereu	1:		SSER	QQAQAEVAVQ	ERN: 18
E._coli.	1:			MKTRTQ	QLEELQKE: 14
T._gondii	1:	MTIEFDV		KSFC	QdFRKECPL: 23
consensus	1:	-----*	-----*	*****	*****: 30

		40	50	60		
B._napus	29:	WSS	REFELT	IRPYTA	DVV ALRGHL	QGVY: 57
A._thalian	26:	WSS	REFELT	IRPYTA	DVV ALRGHL	QGVY: 54
R._communi	29:	WNS	REFELT	IRPYTA	DVV ALRGHL	QGVY: 57
castor_bea	29:	WNS	REFELT	IRPYTA	DVV ALRGHL	QGVY: 57
G._max	11:	WNS	REFELT	IRPYTA	DVV SLRGHL	QGVY: 39
Cucurbita	29:	WNS	REFELT	IRPYTA	DVV SLRGHL	QGVY: 57
P._taeda	30:	WNS	TQLFELT	IRPYTA	DVV RLRLGSL	QGVY: 59
N._crassa	31:	WSD	SRWQLT	IRPYTA	EQHVSKRGHL	IEY: 59
C._cinereu	19:	WKS	PREARVN	IRPYTA	ADVSKRGHL	IEY: 47
E._coli.	15:	WTQ	PRWEGIT	IRPYTA	EDVVKLRGSL	YNPEC: 43
T._gondii	24:	SVS	TSFEVALP	RRLPV	LVSAFRLT	SLHS: 52
consensus	31:	*-*	*****	*****	*****	*****: 60

		70	80	90	
B._napus	58:	ASNem	AKKLWR	TLK	HQVNGTASRTFCAL: 86
A._thalian	55:	ASNem	AKKLWR	TLK	HQVNGTASRTFCAL: 83
R._communi	58:	ASNem	AKKLWR	TLK	HQVNGTASRTFCAL: 86
castor_bea	58:	ASNem	AKKLWR	TLK	HQVNGTASRTFCAL: 86
G._max	40:	ASNem	AKKLWCL	TLK	NHQVNGTASRTFCAL: 68
Cucurbita	58:	ASNem	AKKLWR	TLK	HQVNGTASRTFCAL: 86
P._taeda	60:	ASNem	AKKLWR	TLK	HQVNGTASRTFCAL: 88
N._crassa	60:	ASNAQ	AKKLWR	TLK	EDTFAKRDASYTYGCL: 88
C._cinereu	48:	PSdVQ	GKKLWR	TLK	SEHAKNGTSPSTYTCAL: 76
E._coli.	44:	TLAQ	LGAKMWR	TLK	GESKKGYIN.ELGAL: 72
T._gondii	53:	HSMASRA	PHAGQR	TLK	SLMQKKCVM.LPGAY: 81
consensus	61:	*****	*****	*****	*****: 90

— FROM FIG. 20A (1) —

FIG. 20A (2)

		100	110	120			
B._napus	87:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:115	
A._thalian	84:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:112	
R._communi	87:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:115	
castor_bea	87:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:115	
G._max	69:	DPVQVT	QMAKH.	LD	TVVSGWQCSSTHT	St:97	
Cucurbita	87:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:115	
P._taeda	89:	DPVQVT	mMAKY.	LD	TVVSGWQCSSTHT	St:117	
N._crassa	89:	QPTMVT	QMAKY.	LD	TVVSGWQCSSTHT	St:117	
C._cinereu	77:	DPVQVT	KMAKY.	LD	TVVSGWQCSSTHT	St:105	
E._coli.	73:	TG	QALQQA	KAG	EA	YVSGWQVaa	DANLA:102
T._gondii	82:	ng	TAR	AAEAGF	EG	YVSG	...AALSA:106
consensus	91:	*****!*-*****!***:120					

		130	140	150	
B._napus	116:	NEEGPDLADY	PYDTVPNKVEHLFFAQQ	YHD	:145
A._thalian	113:	NEEGPDLADY	PYDTVPNKVEHLFFAQQ	YHD	:142
R._communi	116:	NEEGPDLADY	PYDTVPNKVEHLFFAQQ	YHD	:145
castor_bea	116:	NEEGPDLADY	PYDTVPNKVEHLFFAQQ	YHD	:145
G._max	98:	NEEGPDLADY	PYDTVPNKVEHLFFAQQ	YHD	:127
Cucurbita	116:	NEEGPDLADY	PYDTVPNKVEHLFFAQQ	YHD	:145
P._taeda	118:	NEEGPDLADY	PYDTVPNKVEHLFFAQQ	YHD	:147
N._crassa	118:	NEEGPDLADY	PYDTVPNKVEHLFFAQQ	YHD	:147
C._cinereu	106:	NEEGPDLADY	PSNTPVPNKVEHLFFAQQ	YHD	:135
E._coli.	103:	ASMYPP	QELYPAN	SVAVVE	INNNTERRAD:132
T._gondii	107:	Cg	GVED	IGILGL	EDFT...EV:124
consensus	121:	*****!!*****:150			

		160	170	180	
B._napus	146:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:175
A._thalian	143:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:172
R._communi	146:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:175
castor_bea	146:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:175
G._max	128:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:157
Cucurbita	146:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:175
P._taeda	148:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:177
N._crassa	148:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:177
C._cinereu	136:	RKQREARMSMSRREER	ATP	VDYL	ICETIAD:165
E._coli.	133:	QIOWSACLEPG	APR	YVDYFL	ELIVAD:157
T._gondii	125:	IS	QAA	SVTST	...BVIVAD:139
consensus	151:	**!*****-*****!***!!:180			

FROM FIG. 20A (2)

FIG. 20A (3)

		190	200	210	
B._napus	176:	GGTCTGGG	TATATVKLCKLFEVERGAAGVHT	AD	:205
A._thalian	173:	GDTCTGGG	TATATVKLCKLFEVERGAAGVHT	AD	:202
R._communi	176:	GDTCTGGG	TATATVKLCKLFEVERGAAGVHT	AD	:205
castor_bea	176:	GDTCTGGG	TATATVKLCKLFEVERGAAGVHT	AD	:205
G._max	158:	GDTCTGGG	TATATVKLCKLFEVERGAAGVHT	AD	:187
Cucurbita	176:	GDTCTGGG	TATATVKLCKLFEVERGAAGVHT	AD	:205
P._taeda	178:	GDTCTGGG	TATATVKLCKLFEVERGAAGVHT	AD	:207
N._crassa	178:	ADTCTGGG	LTAVMKLTKEFEKGAAGVHT	AD	:207
C._cinereu	166:	ADTCTGGG	LTAVMKLTKEFEKGAAGVHT	AD	:195
E._coli.	158:	ADTCTGGG	VLNAFELMKAMTEAGAAVHT	AD	:187
T._gondii	140:	ADTCTGGG	PEMVRRTVFAYNQAGAAGVHT	AD	:169
consensus	181:	***!***	-*****	***!***	:210

		220	230	240	
B._napus	206:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:235
A._thalian	203:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:232
R._communi	206:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:235
castor_bea	206:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:235
G._max	188:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:217
Cucurbita	206:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:235
P._taeda	208:	QA SVTKKCGHMAGKVLV	SVG	SEHINRLVAAR	:237
N._crassa	208:	QAPGTTKCGHMAGKVLV	PTQ	SEHINRLVAAR	:237
C._cinereu	196:	QAPGTTKCGHMAGKVLV	PTQ	SEHINRLVAAR	:225
E._coli.	188:	QLASVTKKCGHMAGKVLV	PTQ	SEHINRLVAAR	:217
T._gondii	170:	Q.RIPKCGHMAGKVLV	SE	SEHINRLVAAR	:198
consensus	211:	!-***!!!!	***!***	-*-!*****!***	:240

		250	260	270	
B._napus	236:	LQ . EDVNGTETV	LVARTDAVAPT	LTIQSNID	:264
A._thalian	233:	LQ . EDVNGTETV	LVARTDAVAPT	LTIQSNID	:261
R._communi	236:	LQ . EDVNGVETV	LVARTDAEAA	NLTIQSNID	:264
castor_bea	236:	LQ . EDVNGVETV	LVARTDAEAA	NLTIQSNID	:264
G._max	218:	LQ . EDVNGVETV	LVARTDAEAA	NLTIQSNID	:246
Cucurbita	236:	LQ . EDVNGVETV	LVARTDAVAPT	LTIQSNID	:264
P._taeda	238:	LQ . EDVNGVETV	LVARTDAVAPT	LTIQSNID	:266
N._crassa	238:	AO . ADVNGSGLT	LVARTDAEAA	NLTIQSNID	:266
C._cinereu	226:	LQ . YDVGVENI	LVARTDAEAA	NLTIQSNID	:254
E._coli.	218:	LA . ADVTGVP	LVARTDAEAA	NLTIQSNID	:246
T._gondii	199:	AASQDCSNG	LVARTDAEAA	NLTIQSNID	:228
consensus	241:	***-***	*****	!!!!*--*****	:270

FIG. 20B

		210	220	230
gi	113033	YLTPTVADAD	ACHGGITAVE	KLTRmTERGA
gi	113027	ELPTIADAD	TCHGGITAI	KLTRLETERGA
gi	2497268	YLRPTIADAD	MCHGGPTTVm	KVARLTAEKGA
consensus		*!*!!*!!!!-!!!!*	*!***!***!*	*!*

240	250	260	270
ACDmTDO	TSTNKKCGHMAGE	CVLPVQEH	VNRLVETRMCA
ACDmTDO	APGTRKCGHMAGE	VLPVQEH	INRLVATRASA
ACDmTDO	MVGCKYCCSLSC	AVLVP	TATHLMRLISTRFQW
!!!!*!!!-*	-!*!!!!**!	*****!***!***!	***!!***!-*

280	290	300
DEMHSGLIVVARDSEAA	TLISSTID	TRD:271
DEFGSNLLAVARDSEAA	TLISTID	HRD:264
DEMGEENLVIAARDSCN	GKLSSSD	PRD:292
!!*****	!!!!!*****!	***!***!-!!!:300

FIG. 21(1)

CCCTATTACGTTTCCTTTTTTTTAAATGCGGCGAAAACATTCCCTCCATAC	050
AGATTTCCCATTCACGTGACGTCTCGCGTGTTCAAACGTCAACTGGTTT	100
TCCCTGCTCTTGTAGTCACAAGACCGTGCAACCAAACCTGCGACACAATC	150
TTGTGCCGTGTGACCACCGCACCGCAACTGCCCACTCTGTAAACATAGTCC	200
CTCCCTAAACCGTCAAAACCCCGAAACGAACCGGATGCTCTTCTCTCGTC	250
CTTTCTCCCTCGTTTTCTTTCTTAGAAAAACAGGAAAAATCCTCACTGGA	300
TATGTGCACATTTACCGAAGCGATGCGGAATCCACGGCGAGGTGGCGGGT	350
CAACTCCCTTGGCCAGGGGTGAGTCTGGTAGTGGCATTTTATGGCGTAG	400
AGACAAATGTAAAGGTCTCCCATTTGAACAGAACCTGCTTACTCCTTCGTCT	450
TAGCCCCCTCAATTCTGCATTTACAATCCCTTTCAAAAGCAACAAAGTCTT	500
ACATCCAAAACCCCTCCAAAATCCCGTGGTGTGTGACCTTTCCAGTGACTC	550
TTGCTCCCACAACCGTGCGCCCTTTTTCGCGGCTTGCCGAAACATCGAAA	600
AGCTGCGTCGCTCGCATTACTGCTTTTTGGGCCTTCACTTTTCCCCAAAT	650
ACCCTCCGAGTTCTATACGTTTCTTCGGTTTTTGCTAAGCCACAAACTGC	700
AGGCTTAGCAGGCCACCTTCCGTCGTGAACCTCGTTCACCGAGTTACCGGC	750
CTCACACCTATTTTCGTTGCCGTCTGGAAGTCAGTAAGGGACCACCTT	800
CACGTGCAGTTGACCGGTCTGCAATGACCATTGAGTTCGATGTCCCGAAA	850
TCCTTTTGTTTTGATTTCCGCAAGGAGTGTCTTGAACCACTGTCCGTGTC	900
TACTTCCTTTTTCGTGCGCCTTCCGCGCCGTCTCCCCGTCTCTCGTCTCGG	950
CCTTCCGTCTCACAACCTCCCTTCATTCTCACAGGTGGTGTACTGCAATC	1000
ATAAAGAACTTGCTGTCTGCACCTCTTATGCAGAGTCATATTCAGTCTC	1050
CTACGGAATATCATGTCCACAAATAAAGAAAACCTGGTTTGATTGTATCTC	1100
ATCACTGACTGTCTCGTCCGACCCTTCCCCCCCCATAAAATAGCTGCTAACG	1150
TGCAATGATTGAGATACATTTATCTACCGCACTTTAGTTTAATACCCCG	1200
GTTTGTGGTTAGGGTTGTATGAACGCAGGAATACTTGTAGATCTTTGGAG	1250
CTTAAATATAAAAGATGCATGTTTATATGTGAATCTTTCAATGAAAACAT	1300
GTACGTGCATCTACACGTCTTGAAACGTAGGTGTACAACAATGTGCTTGG	1350
GAAGTCACTGCCTCTCTACAAATCACATAGTTTCTGTACGGTGGCGCCTC	1400
ATTTTCTTTCTTTGACTCTCTGTTTGGCGTGTCAACATGATCTACCCCTCGA	1450
TCC'TCCCAACAGTCCTTTTCGCTGTGCTTATCACTCTTTTTCTTTCAGTCC	1500
TTTCTTGCTGTGCTCGTCCGAATTGCCTATTTCTCTCCACTCTTTCTCTT	1550
CTTCTTCCCTGACGTGGTCTTGTGCGGTTGTCCGGGTTTCCCTCTGTCA	1600
T'TT'CCTAACCGCTGCCTTCCCTCTCCTGTTCGCTGCAGCATGGCGTCTCG	1650
TGCTCCCCATGCTGGACAGCGC'TT'GCGCAGCCTCA'GCGAAGAAAATGCG	1700
TCATGCTTCCCTGGGGCTTACAACGGTCTCACCGCGCGCCTCGCGGCTGAA	1750
GCAGGATTTGAAGGAGTCTACGTCTCTGGAGCTGCTCTCAGTGCATGCCA	1800
AGGCGTCCCCGATATCGGCATATTAGGTCTCGAAGACTTTACTCGAGTAA	1850
TCTCCCAAGCCGCCTCTGTCAACAGCCTCCCTGTTCTCGCCGGTGCCTAG	1900
CAGAATCGTGTTCTTCACTTCTTACTTCTATCTGCTTTGTGTCTTTCTTG	1950
TTTTTGGTTTCGACTTGCTTGTGCTGATGGATAGAACCCACGTTGGGTGTTT	2000
CGACGCGCCTCGAGCTTCTTCACTTGGCCCTACCTTCTGTACTCTTCTCTGA	2050
CTTTCGCTTCCCTAGTCTCGAGGATCCACGTGCGTTTTTCGACTCGTCCCTTG	2100
TCGCCGTATCGCTTCAGAAACCGTTCACATCTACTGGCCCTTCCCTCGTC	2150
TTTTCTTTTCTCGATGTCCTTTTCCCAACTTTTCGCTCTGCTCTCTCTC	2200

— FROM FIG. 21(1) —

FIG. 21(2)

TCCTCTGTCGACGGTCTGGTCACTCATTTCGTTTCGTGTCGCGTTCCCGTT	2250
GTGCTCTTTTCTCTCTTCTTCTCGTCCCTCTCCGTCTTCTCGCTCTCCTG	2300
TTCTCCTACCCGCTCTCCTTTTCTGTCTCGTCCGCTCAACCTCTCTCTCT	2350
TTTCCGAGCTCTTGCTTAGATGCAGACACGGGGTTCGGTGGCCCTGAAAT	2400
GGTTCGGCGCACTGTCTTCGCGTACAACCAGGCGGGCGCGGCTGGGCTGC	2450
ACATTGAGGACCAGCGTTTGCCGAAGAAGTGCGGGCATTTGGAGGGGAAG	2500
CAGTTGGTGTCCATTGAAGAGATGGAGGAGAAAATCAAAGCGGCCGCTGC	2550
GGCGTCCCAGGACTGCTCGAACGGCGACTTCATCATCTGCGCTCGCACGG	2600
ACGCCCCGAGTGTCGACGGTGGGTGACCCTCGAAACGGCCGAAAACAGAA	2650
CTCTAGGGTCTCGCGCATTACAGCGCGGGTGTCCCTCGAATGGACGCTAC	2700
AGTGCTGTTAGTGTCGAGTGTCTTTTAGCGACTTTCTTCAGAGCTCACTTA	2750
GGTTTCGTACGATTTCAATCGACAGACGGAAAGACGCTCAAGTGAAATTC	2800
GGGCCACCGAGAAGGCGAAGAGAGAGCAGAGGAAGGGAGGACCGGGAACC	2850
TTTGGACTACTGAGAAGCAGGCGAAGACGGGCGTTTCAGAAGCGCCTGAG	2900
CAGGTCTCCACACCGAGAGAAGCAGACTGAAGACGCAGTTCAGATGAAGC	2950
TGAAAACCGGAAAGCGCCTCTTTAATATTGTAGAGGGAGTCTTAAGTCG	3000
TGCCCTCTTTTCTCCCTGTCTTTCTCGCTGTCTCTGCAFGGCTCAGGGCTT	3050
GATGCGGCTGTGGAGCGAGCAGTCCGATACACGGCAGCCGGAGCAGACAT	3100
GCTTTTCCCCGAAGGACTGGAGACAGAGGTGAGAGGTGGAAAGAAGAATC	3150
AGAGGAAGAAGGCGTCGTATTGGAGAGGCAGCGAGAGGCAGTCGCTCTGG	3200
TGAGAAGCTGCGGCGGAAAGGGAGAAAGAAAGAAATGAAAAACCCGGT	3250
CGAGAGGGATGGAACCTGAAAACCTCGGAGAAGTGGAGAAAGGGAGCTAG	3300
GAGCAGAGGAGGTGAAGGAATCCGTATAGTGGATTGATGTGTGACGTCAA	3350
CTATGAAAGACATGACAAATTCAACTACAGGCGAAGGGTATGACAGGGAC	3400
ATGCGTTTTGTACAGAAAACAGAGGACAATGAACATGTCAGACCTCATA	3450
CACACGCGAAGAGATGCGCAGTGGATTATGGAATGAGCAAGAGTAAGGAG	3500
TGAAACTTCACAATGTGCATTCCGTGTGAGTTGAGTCATCAAATCTCGG	3550
TGTTTCGTGCTCTTTTCTCGTCTGCCTCCAAAAGTGTGTCTTGCCTTC	3600
CTCATGTCTGCTCTGCACCCATTGTCCTTACCCTGTTCCGTTCGCTCCC	3650
CGTATGCCTGCGGTTTCTTGTCCGTTATCAGTCTCTACCGGGTTCATCTC	3700
CTCTTTCTGCGGAGAGGCTTTTGTCTAGCGATGGGTGTATGAGTTCGT	3750
TCTGTCTATCCTCATATACCTACCGTCACGAGACAAACAACCTGCTCCATGGT	3800
CGCTGTACACGGCCAACCTTGTGGGCTGCTCACAAAAGCCACAAGTGTCTG	3850
AGTTTCAAAAATTCAACCACATTAGTGTGTTCACAGTTCGGTTACGTTTAC	3900
GCGTTTCGCGAAGAAGACGAAGACGAAAGACGCGTCCATTTTCAGAGAAGA	3950
CCTGTCCGTTTTTCGTTGTGACACCAGGAAGAGTTTCAAGCATTTCGCGAT	4000
GCATTGGCGGTTTTTCCTGGCAAAGCGCCTTTCGGGGGGCCCTATCTGCT	4050
CGAAAATATGACGGAATTTGGAAAGACGCCCATCATGGAGCTTTCACCT	4100
TGGAAGGCCTTGGATACCACTGCGTTATCTACCCTGTTTCACCTCTCAGA	4150
GTCGCCATGAAAAGCGTCAAGGTACGTTTGTCTGCTATCCATACTGAGT	4200
GACTCGGATCGATTTCTTCGTTTGTGTGGCACGTGGAACCTGAGTGCCAT	4250
ATGCGTGTACGCAATGCAGAGGAATGCATGCATGTGAGCACACCTGTCT	4300
GCAGCTACGCGAATCTCTGCCTGTGTTGACCTTCTACCTGATGGCAGGCA	4350
TGCACGTGTATACACGCACAAGCATCTGTATAAATATGTGTAGTTGAGTA	4400

— FROM FIG. 21(2) —

FIG. 21(3)

ATTATACGTGACCTATTAAATCTAAAGCAGAAAACATGCTCATACCGTTC	4450
TTGT'TGTTGCTCAGGGCATGCTGGTCGACTTACGCAAGAATGGCAGCGT'T	4500
GGCCATAGCCTGGAGAAAATGTATACACGGCAGGTACAGCGTTACCATCA	4550
TAAGGCGGATACTTATAAGATTTTCCCTTCAATGACGTGCATGCATCACGG	4600
ATACCAAACCTGCTCGT'TTAATCCTCTGTTTTGCTCTGTAAGCGTCTTCC	4650
TTCTTGTAATTCTTCCATCCTTTTCATCTGCCGTTGTGTCAATTTCTGCCCT	4700
GGGGCTCTGTCTTCGCTTTAATGCCCTCAGTGTTTTTCTTCTTTCTTGCC	4750
TCTCCTTATTCTGTCTCACGGTTCCTGTTTGTCTTCTGGTATCTCGTGCT	4800
GTTGCTGCTTTTAGGAGCTTTATTCCACTCTGCACTATCGGCCGGAAGGG	4850
ACGTGGACGTATCCCTCAGCGAGTGTGTGCATGGACAAAGCCGTGGAAGA	4900
TACCGAGGCCTAGGGAGTCTCAGGCTCGGCATTTTCTTTTCTCGACTGG	4950
TCTCACCAATACAAAAGACAATGCTCACAGACGAAAAGCAGAAGTTCTGA	5000
AAAGACAAAAGGACGAAAGCGAGGAAACATGGCACACGACGGCGGGGGGA	5050
CTCTCAC'TGCACAACGTTATTCCAACCAAGTGTGCAAGAGTACCCGGATG'T	5100
CCTTTGGTGTATGAATGCATGGTCTTTTTCAATTCCATCTGGCTGCTTCC	5150
GTGAAATTTTCGACGAGAAGCAAGAACAGAAGGCGAGCTTTTGTCACTGCG	5200
GCTAGTCGCCAATATTGAAGGGCCCGGGGGGGGGGGAGCAACACAAACC	5250
ACAGAAAAGGAAGGCGTCTGCAAAATTTGCGGCGTCCCTCTTGGAAGAA	5300
AGAAAACCGAAGAGGATGGACAACTTACCCACCGAGGACAGACCACAGA	5350
TGCGAAAAAGAGAATGAATCGAGAGAAAAGAAATGCGAGCCGATGCAGAG	5400
GGGTCTCTTTCGTTTGAGGAGTTTCCAGGAGGGAAGCGAAAGAGACGTTT	5450
GGAAACCGGAAAGTGGACAAAACCTCCTTTAAATGCGGAAGAGTGAGGCG	5500
AATGCAGGGCGGCTGTCTGTTTCTCTTACGAAACTGTTCAAGGGTTAGA	5550
AACCCAGTAGAGTGCTCGTGACATCTTCCACTTTTCGTGTCTCACTTGGG	5600
TGCTCGGTTTCTGCAGTGCAAGCTGCTTCTCGCTGTCTCACTTCTTCT	5650
ATTGAGTAGACGAGGCACAGCGACCGGTTCTGCCTGCGCGTTGTGTGAA	5700
AGGGGAAC'TCTGAGAGGCGTTGTTCTTTATGTTTTCTAACTGGTAGAGAG	5750
GGACGTGGTAGCGTGAAAAAACCGGCGTTTCTTTTGCTTCACGGCAGCAC	5800
ATGAGAAAGCTTCGGAGGTAGATGTGTTTTCGTCTAAATGCATTTCTCG	5850
GAAAAGAACGCCAGAGAACGGTAAATTCCTCTAGACAGTGAAGAGTGG	5900
ACTCGCACT'ACCCTCCGCCGCGACTGCGTCTTTTCTCCACTCTGCGAA'I	5950
CTCACTTTTCTTCTGAATTTCTTTGTGCGACGAGGAACCGACCGGTAGAC	6000
GGCGGCACAGCGTTTCTAGCAGATATTCCGGTTTGTGTGATTAGTGTCT	6050
GTCTCTTTCTCTCACTCTCACTTCTTGCCCGGAAGGAGGAACGCCGCAG	6100
AAAAGCAAAAACACCGGCGAGTGGACCCAGTTTTTCGGTAGCTTCAGCTGA	6150
GGCCCGCCGGTCGCGAGCGAAACTTCTCGGATTTATCCTCCAGCACTGAC	6200
AAAACCCTCTGGTGCAGATACGCAAAATGCGCATGCACGTGGAAGACGTCA	6250
AAGATATCCTTGCGATGAGCACGCAAAAGAGCCTGGAACGCATGCGCTAG	6300
AAACCCGCGAAGCACCCCAAAGTCGGCAATCTCTGTCTCACGTGCACACC	6350
ACCGCGATGACCACGGGAAACGGGACAGACTCTACAAACCTCCAAAATCT	6400
CTGTCCGACACCAAAAAAACAACACGGATTCCCGACGACAAAAAGACTC	6450
TCAACATCACATCCATGTGTGCATCTCTCTACACACTTGTGGCGGAA'AC	6500
ACATTTGTATCCATACATATACTTTCTAGTCGCGCTGCAGAGAGCTCCG'I	6550
CGGTGTTCTTCTTCTGATCGGAATGGCCTCGCTAGCGAGAGTCTTTGCCA	6600

— FROM FIG. 21(3) —

FIG. 21(4)

TTTCGCCACTTTTCCCTCTCTAGTTCAAGGTCTGAAAAAGACCATTTACG	6650
TTTTGAACTCTGCTCTGTCTCTCGGATCGCTCATCTGCTTTCCAGCTCCC	6700
TCTCTCCGCACATAAGCCGAATGTCATTCTCTCCTCTCAGTCTGCCC'TTG	6750
CCCGGCTTCCCAGACGAGGGGTTTTACGAAAAAATGCCGCCTCACCGTCA	6800
GAGCATTTGCTCCACACCTTCTTCCGCTGGCTTTCCCCTCTGCTTCTCC	6850
GTGTTTCTCTTGATTCACTTTTGCCTTCTCTCTTGTCTCCGCCCCGTCTG	6900
CGCGACCGCTTCAATCTAGGAGAGGCACACTCCCCCGAAAGAGCGTGTT	6950
GCTTTGCGCCTTCTCCTTCTAACTCGCTTTCCCCACAGGAGGCAGTTAAG	7000
AAGAATCTCAAAAGGATCCCAGAAGACACCCTTAGAAATCTCGAAAAAAC	7050
GCTCAAGAACCTCAGAAGAATCTCTCGGAAACCTCAGCAGAACCCGTCAT	7100
GGAGCTCTCAGAAGTTTCTTCAGAATCTCTCTAGAGGAGA	7141

FIG. 22

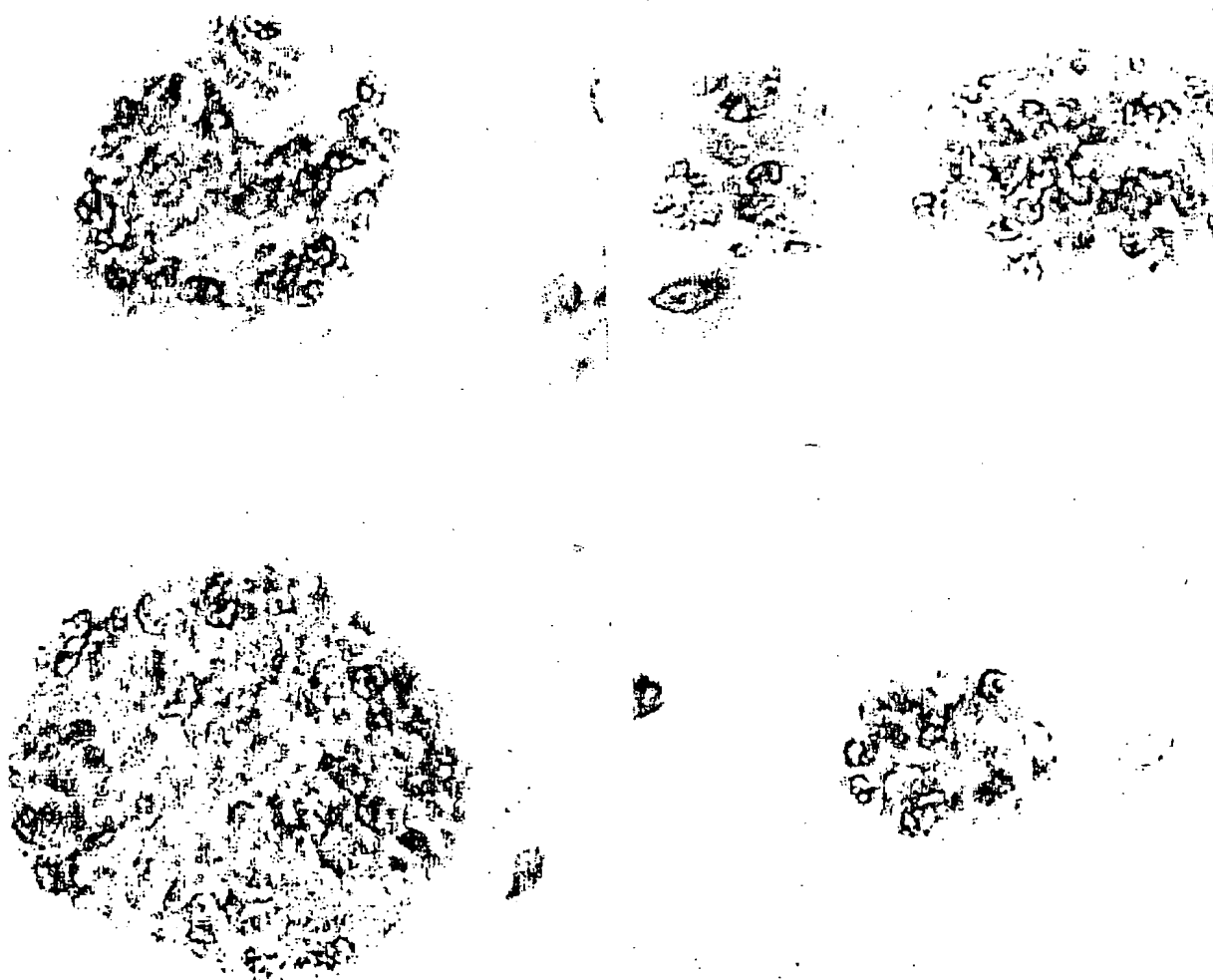


FIG. 23A KEY

- 1 = Cotton lysate + rabbit anti-ICL
- 2 = *T. gondii* lysate + rabbit anti-ICL
- 3 = Cotton lysate + rabbit anti-MS
- 4 = *T. gondii* lysate + rabbit anti-MS
- 5 = Cotton lysate + rabbit pre-immune
- 6 = *T. gondii* lysate + rabbit pre-immune

➡ indicates ~ 60 kd proteins reactive with anti-cotton isocitrate lysate (ICL) or anti-cotton malate synthase (MS).

⬅ indicates *T. gondii* protein reactive with anti-cotton MS.

FIG. 23A

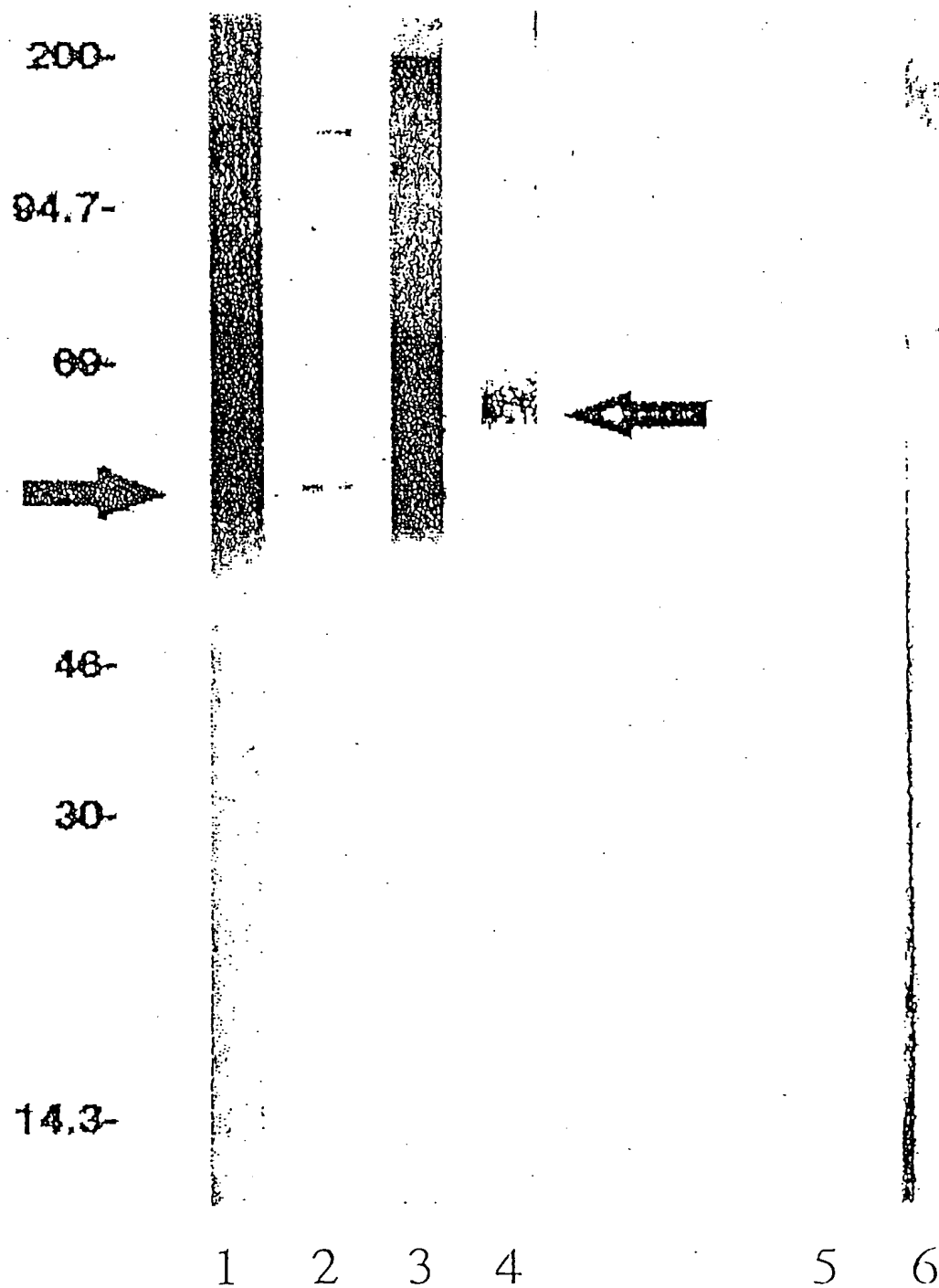


FIG. 23B

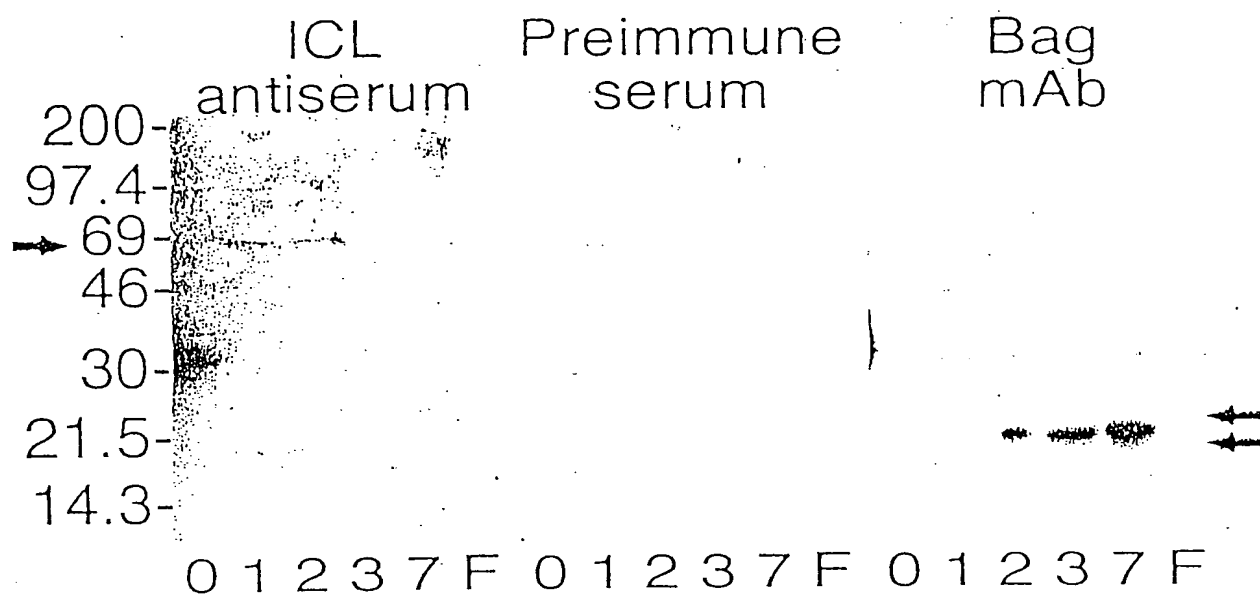


FIG. 23C

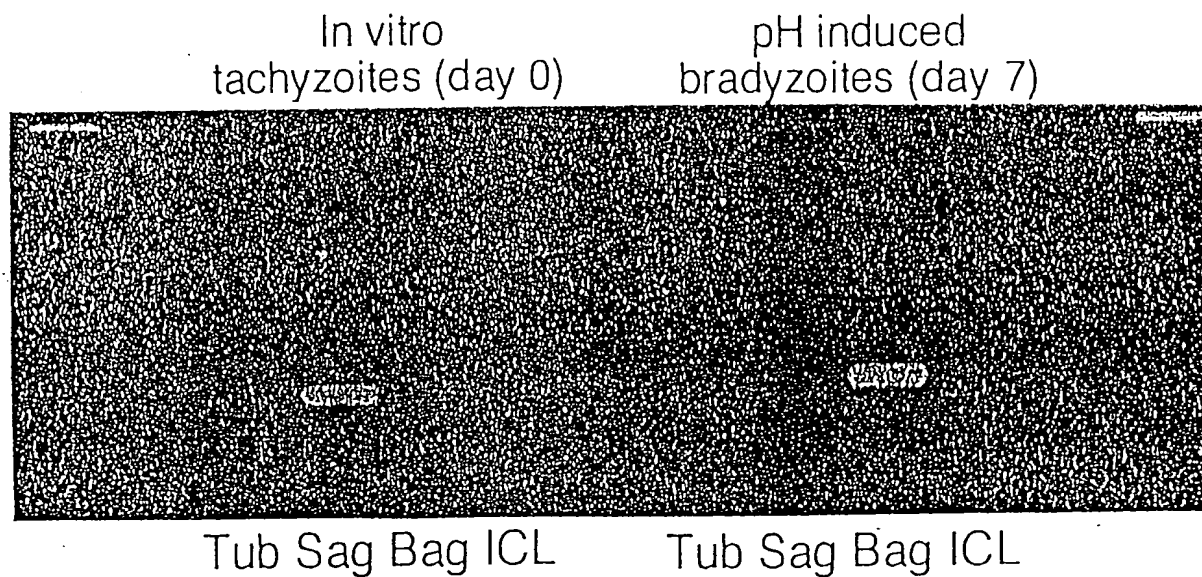


FIG. 24A

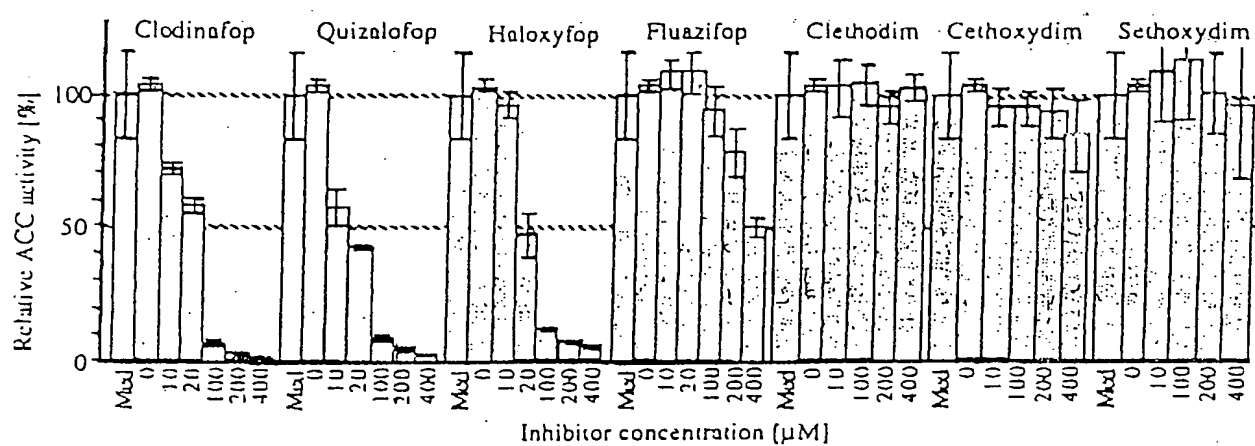


FIG. 24B

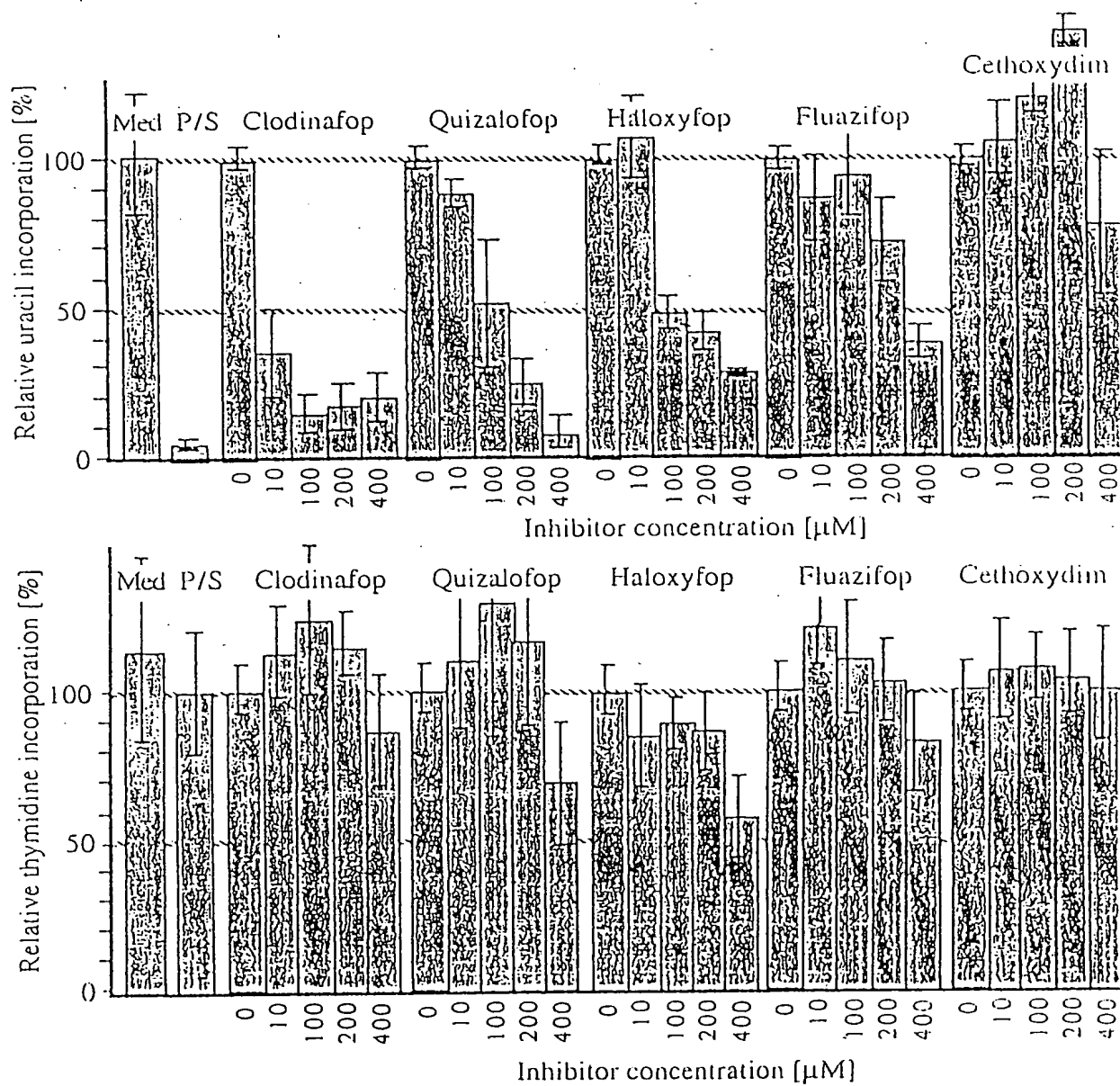


FIG. 24C

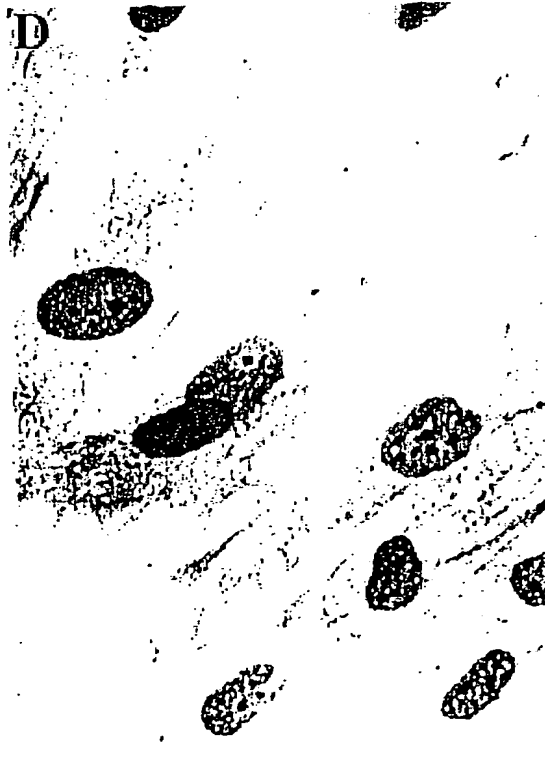


FIG. 24D (1)

LOCUS AF157612 5258 bp DNA INV 10-NOV-1999
DEFINITION *Toxoplasma gondii* acetyl-CoA carboxylase 1 (ACCI) gene, partial
cds.
ACCESSION AF157612
VERSION AF157612.1 GI:6164685
KEYWORDS
SOURCE *Toxoplasma gondii*.
ORGANISM *Toxoplasma gondii*
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; *Toxoplasma*.
REFERENCE 1 (bases 1 to 5258)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Growth of *Toxoplasma gondii* is inhibited by
aryloxyphenoxypionate herbicides targeting acetyl-CoA
carboxylase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)
REFERENCE 2 (bases 1 to 5258)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA
FEATURES Location/Qualifiers
source 1..5258
/organism="*Toxoplasma gondii*"
/strain="RH (EP)"
/db_xref="taxon:5811"
mRNA join(<1..90,547..702,2442..2672,3066..3421,4267..4582,
4941..>5258)
/gene="ACCI"
/product="acetyl-CoA carboxylase 1"
gene <1..>5258
/gene="ACCI"
CDS join(<1..90,547..702,2442..2672,3066..3421,4267..4582,
4941..>5258)
/gene="ACCI"
/codon_start=1
/product="acetyl-CoA carboxylase 1"

— FROM FIG. 24D (1) —
 FIG. 24D (2)

/protein_id="AAF04493.1"

/db_xref="GI:6164686"

/translation="RVLIANNGMAATKSIFSMRQWAYMELGDDK
 LLEFVVMATPEDMRANPEFIRRADKIVEVPGGPNRNNYAN
 VDLICQIAVQEKVDAVWPQWGHASENPNLPRRLSELGITFI
 GPSATVMAALGDKIAANILAQTAGVPSIPWSGDSLKATLDS
 TGAIPRDIFDQATVKSVEECEK VADRIGYPMMIKASEGGGG
 KGIRMVDRKEQVRGAYEQVVAEVPGPSVFMMLCTAARH
 IEVQIVGDEDGQAVALSGRDCSTQRRFQKIFEEAPPTTVVPP
 HTMKEMEKAAQRLTQSLGYVGAGTVEYLYNRKDDKFFFL
 ELNPRLQVEHPVSEGVGTGVNLPAAQLQVAMGIPLWRIPDIR
 RFFGRDPNAGDRIDFINEDYLPIQRHVLASRVTAENPDEGFK
 PTSGRVDRLFEQPLENVWGYFSVGASGGVHEYADSQFGHIF
 ATGKNREEARKKLVLGLKRVDVRGEIRTPIEYLVQLLEDKD
 FIENRIDTSWL"

BASE COUNT 1176 a 1271 c 1351 g 1460 t

ORIGIN

1 cgcgtcctca tcgccaacaa cggeatggca gccaccaagt cgatctctc catgcgtcag
 61 tgggcctaca tggaaactcg cgacgacaag gtgagcctga cacagtgaac aaggltggatc
 121 tcttgtagc ttcgaaatg ccatactctc aaaaattga agagctgacc tgacgcaaaag
 181 ctaaataatc atgaagactc tctgtcacc gtagtggtat tccgttttg tcttgccccg
 241 ctctctatct tgttttcgc cgcaacagag aactgtaact gtatatacag tgatatatat
 301 agttatatgt acgtgtttt tatgcgcgta tgtgttcagt cacaactaca aaataaatgt
 361 acacgtacat gcttagatag ttacgtggcg acaaacctct tctgttcag ctatgcgaat
 421 cgcgcgaaaa ggcgaccgag acatgaagct ctcttccttc gcatttctag catttgcat
 481 cgcgtatgtg ggtcgtgtgg aactgagtg gcagaggcat gtttgtgtat gtttttgt
 541 gtgtagcttt tggagttcgt lgtgatggca acccagaag acatgcgagc gaactctgag
 601 ttcattcgcc gcgcagacaa gatcgtggaa gtccagggg gtccgaatcg caacaactac
 661 gcgaacgtcg atttaattg tcaaatcgct gtccaggaaa aggtgaggga gacgcaatgc
 721 ggggtcgtcg ctgcttctg gtggacagtt taaagagcga attcattcag atggatagtg
 781 cgactcagaa gctcgaag tgctgccttt atccagaggt cattaggtct acaggacctt
 841 ctgacgttca cactgagata ctacacgtct tctcagttg gaggttctt gtttctct
 901 ttctatctct attcttcgct ttttgcctc ttccctgtg ctagtcttc cgtgttcccc
 961 cattttcaag tgcgtgtatg tctctctcat cactgcgtg gcgctgcgtt ttccgttgga
 1021 agggagaaga ctctctcttg ttctctctc cgtgtctcg gctctctcg actcttgcc
 1081 ttctttctg agaaggggaa agagttgggg aaccgagaa accggcgaga agacggcgca
 1141 tgagtgaagc cccggaaaac gggttccctg tcttcgggt gctctgtct tcttctctt
 1201 ctgcctattt cagcggatag aaaacgatct gcatagtcc tcttgaggtg gtccgtctt
 1261 aagctgtgga gttgtgcat gcagttccac agtgggcgtc ctctggagca gcagacctac

— FROM FIG. 24D(2) —

FIG. 24D(3)

1321 cctcactggg tctccattga tctgaacaaaa ctctcatgeat ttccctctcaa ctctctcttc
1381 ttccctctcg gcatcglttt gccaggacct cctgtccitt caagaacac gcggcaggga
1441 ggcatltgat ggatcaclat gtcggltgat gatgtgtgg aagagtlactt gcegcgttac
1501 tgtacaacct ctatcgtaca tgttagagga gaaaacggat ctctctctgg aggtacccegc
1561 tctctgaaat ctatcgtct atccgattt tagggcgagg ttagtgaagc acgcgcgcgt
1621 ctgtctgggt gctctgtatt ctgtttttg gcaagacgat ggaggatgaa cagagggaat
1681 ttgtcact accactgacg agccgagagc tcatgattg gactgtccc tcatgtaaat
1741 ctgacgcgtc gctttatag cgtttcgtc ctgaagcga tctctctact ctctaggga
1801 ctctctcat ggcctctct ttgactgtc gggattccgt catcgttct gttgacttcg
1861 gctactcacc ttctcccag tgtgcgtgt gtccgaaact cgtttgtt tactttctg
1921 tgtctctgga gacaaggatg aacagaggat tctattgtca ctaccactga ggagcaacca
1981 gctcgtgat tggacttcc cctcattac atctgaggct tctctctga aacattcgg
2041 ttctactt ctgttcgcga tgcctcggg gctcgcgg acgctctag cttaaccgc
2101 ttctccgcc gccctgtgc ctgttttct ttgcgtgggt ttccctctc atggccgccg
2161 ttgatcat cgcgttct ttccggatc ttctgtctc taattcaat caacatgagc
2221 tgttttcc tgtccgtct cctgtttt cgcgcgcata cccacgacga gcgcgaattg
2281 cgtcaagccc tccggtgtct cgtttcgcg agccgtgtct gttctgcctc ctctgcctc
2341 cctttaccg cgtctactg ttctgcgcg tcatctcgt ctgtctctg tctctctc
2401 ctgcatttt attccactc tgttttgcg tcttcttta ggtggacgca gttgtggccg
2461 gatgggggca tgcacggag aatccgaat tgcctcgtc ttgtcggag ttggggatca
2521 cgttcattgg ccttagtgca acagtatgg ctgtctctgg agataaaatc gcggccaaca
2581 tctcgcgca gacagcaggc gtccgagca ttccctggag tggagattct ctaaggcga
2641 cactcgacag caggggcgc attcctcgc atgtaagcag gcgtttac tatggacata
2701 atagacccct ttgagttc gactcttcc gatgtatcc attcaggggc tctctctga
2761 ctctataagc agaaacgat gaacggacaa aaggaacgtg aagacctag acagggtaac
2821 atgcgcata atatatatat atattatat atacatatat ttatatatat atatatatat
2881 gtgaatgtct gaaaatgcc gttctcgcg gtgttattt tgtggcaaca tgtatatata
2941 tataatgtat tgcatacaca tataaatata tatatatata tatatatata tatatatata
3001 tataaataaa tatatgcaga ttgtgtatg tgcgtgcgga ctgcgtgtt tacgtttgt
3061 tttagattt cgaccaagcg acagttaaga gcgtggaggga atgcgagaag gtggcagacc
3121 gcattggta tccgatgat attaaagcga gtgaggagg cggtggaaaa ggaattcga
3181 tggtcgatc gaaggagcag gttcgcggg cgtacgagca agtcgtggct gaagtcaccg
3241 gatctctgt ctctatgat caactctgca ctgccgcgc ccatatcga gttcagattg
3301 tgggggacga agatggacag gctgtcgtc tcatgtgcc cgactgcagc acgcaacgac
3361 gcttccaaaa gatatgtga gaagcaccgc cgacgactgt cgttctccc cacacaatga
3421 agtacgcaag agacacgac cggaacaca aaatcctgca acgcggaaag actgggagga
3481 cacagcccg aggagaagaa aaacaagaac gataaaggag ggggaaagcc aaggctaggg
3541 agaaaacgaa caaggataag ggaaggagga caacgaggag aaggggagga acagggcagt
3601 gaagacgaga gcacgaccgc tgaaccaag atcgggtc gccctcgggt tcatggtgt
3661 gtgactctt cgcgaggcgg gtcgagtgt tattgtctg aggcgttct cctgagggt

— FROM FIG. 24D (3) —

FIG. 24D (4)

3721 cagtgcctaga gagggacgga aaggatgaac gagttgacgt tcaccgttgc gcggagagtg
3781 aaaaaaaaaag actgccttgt ggggtgtcca ccttctcca aacgtcgcgg cacatttta
3841 agccttccag tggccactct aaaccacgcg aggggtcaagc aggtgtgcaa cagagatctg
3901 ttctgtcag tcttgcctc ttactccttt ctcttctccg agagagaaaa tggaacggag
3961 gcagtatccc gagatcgaca gaatggcttc gcatctcgt tegtcttct cctcacttta
4021 tcggaaagtg ctctgaaaga tccitgaagg cgagagaggg cggaacggtc cgcgaactct
4081 acttgccttg cgtgattgt ctgccgtgag tgactctgtt gtcctgtgt ctctggctcc
4141 ccgcttagcg gglttccctt cgattcgtcc aagagagtta ctgtgggtgt tctcccagca
4201 tccgctggag acctggaagc gcgctcttcg tcttcacagc gtctttgac ttgttctgt
4261 tcgcagagag atggagaaag cagctcagcg cctgacgcag tctcttgggt acgtgggcgc
4321 cggcacctgc gagtacttgt acaatcgaaa agacgacaag ttttcttcc tcgagttgaa
4381 tccgagactg caggtggagc atcctgtctc ggaggggcgc accggtgtca atttgcgcgc
4441 tgtcagctc caagtggcca tgggaattcc tctgtggcga attccagata ttgcctgggt
4501 ctgtgggcga gacccaaacg caggcgaccg catcgatttc atcaatgagg actacctccc
4561 catccagcgc catgtctctg cggtagcaaa ctggatgcaa cgaacgcctg cgcattgagc
4621 ttctacgtg gtgtctctct cgatactact aaaaagtgt catgcggaca tgtgcagttg
4681 tgtgacgttg agtcgcaatt gtaactgaaa agaagtcata aatatcaaa aactgttca
4741 atactgtccc acgtaccgat acacacatac acatacttaa tatatatata tatatagctg
4801 catacgtact tcaaatacat acatacatac atacatcgat acacatgata tatatatata
4861 tagatatata tggtttttgg ttccctttgg ttgagcgggt ggaagtgac ggattgatt
4921 ggaagttctt ttgttttcag tctcgagtga cggcggagaa tcccagcga ggattcaagc
4981 cgacgagtgg tcgcgtagat cgccttggaat tccagcctct ggagaacgtc tggggatact
5041 ttccgtggg cgcagtgga ggggtccacg agtacgcaga ttctcagtt gggcacatt
5101 tcgcgacggg gaagaatcgc gaggagggcg ggaagaagct ggtgtcggc ctgaagcgcg
5161 tggatgtccg tggcgagat cggacgcaa tcgagtactt ggtgcagctg ctggaagata
5221 aagactcat cgaaaaccgc atcgacacat cgtggctc

— FROM FIG. 24D(4) —

FIG. 24D(5)

LOCUS AF157613 6965 bp DNA INV 10-NOV-1999
DEFINITION *Toxoplasma gondii* acetyl-CoA carboxylase 2 (ACC2) gene, partial
cds.
ACCESSION AF157613
VERSION AF157613.1 GI:6164687
KEYWORDS
SOURCE *Toxoplasma gondii*.
ORGANISM *Toxoplasma gondii*
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; *Toxoplasma*.
REFERENCE 1 (bases 1 to 6965)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Growth of *Toxoplasma gondii* is inhibited by
aryloxyphenoxypropionate herbicides targeting acetyl-CoA
carboxylase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)
REFERENCE 2 (bases 1 to 6965)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA
FEATURES Location/Qualifiers
source 1..6965
/organism="*Toxoplasma gondii*"
/strain="RH (EP)"
/db_xref="taxon:5811"
mRNA join(<1..39,412..600,902..1222,2554..2783,3357..3531,
3981..4130,4687..4812,5274..5360,5770..5826,6311..6426,
6938..>6965)
/gene="ACC2"
/product="acetyl-CoA carboxylase 2"
gene <1..>6965
/gene="ACC2"
CDS join(<1..39,412..600,902..1222,2554..2783,3357..3531,
3981..4130,4687..4812,5274..5360,5770..5826,6311..6426,
6938..>6965)
/gene="ACC2"
/codon_start=1
/product="acetyl-CoA carboxylase 2"
/protein_id="AAF04494.1"

— FROM FIG. 24D(5) —

FIG. 24D(6)

/db_xref="GI:6164688"

/translation="RILIANNGTAAVRCIRSMRHWAYEALGNSKALEFVVMATAA
DIDANAEFIAEADFYVEVPPGPSNNYANLHLIVQTAETYECD
AVWPGWGHASENHRPAILQTLKRKTIWIGPSPQAMLALGDK
IGSAVIAQSVNVPCVPWSGETRSPKRADTQPHSKTRRSISPPHFH
TRESMHLSISVSKVFLTCLWTHFAFPLHQVLDCCAKIGYPVMIK
ASEGGGGKGIRRVTNAAEEVADAYRQVVNEVKGSPVFVMRMVS
DCRHLEVQLLADKSGRCVSLGSRDCSIQRRRCQKIIIEGPVVAAP
PEVVSQMEDAACRMAMAVGYENAGTCEFLYDPKTHQFAFLEV
NARLQVEHVVTCEVGDENLPAAQLQVAMGILIDDIPDIKAYLD
SAASNKPVGKHIIAARITAEHAEESFRPTVGLVHELTFRPSRFVW
GYFSIGSKGNIHAFNDAQFGHLFAHGKDRREAVKHMVLALKD
MTIRGELRTNVEALIKILEHPDFVANETHHTWL"

BASE COUNT 1683 a 1627 c 1841 g 1814 t

ORIGIN

1 cgcacccca ttgccacaa cgggactgcc gctgttaggg tgagtgtgt ttctcatgc
61 agcgtgtgag tacagagccg cgagctttt ttctgccaa ctctctctcc aaattccctg
121 aagtcaggga agtagagcgc cggcacgccc ggggcgcggg gaaaggggga gaaagcggcg
181 agagaaacgg gggcggaagc ggggagccac aagcacagga ctctgcgaaa aaaacggagc
241 tctgcaggca aggcgggaga ggaacaagaa gggaggaaag cgaagggtga agggcggggc
301 aagaattatg acaaggggac gagaagctgg agggagatct gcagcgcgaa gctgtcgaaa
361 acgcaatcat gttgccgacc ctggagtgc accctccgc gcttctgca gtgcattga
421 agcatgcgtc actgggcgta tgaggcgcic gggaacagca aggccctega attgtcgtg
481 atggccactg cagcggacat cgacgccaac gctgaattta ttctgaagc agactctac
541 gtggaagtc ctcggggcc gaactcgaa aactacgcca atctgcatt catgttacg
601 gtaaaagta cggaacaggc caaccgaacg ccggaggaa cgcgacagcg gcgtcgtct
661 ccatacgccg agagcgttc ctctacacg cctgttccg atttcggcg ttgcagacag
721 aggaccgcgc agaacgcggt ggacgaacc cagttcacc gcacaacggg agccgtcgtc
781 agtagcggac gaactctagc gtgcctgcgc agtcaatgt aggcattccg acgtgaggac
841 gctctgtgcg ggtgcgactg gtctgaagc ggcgatgcgt tgattttct tctttcgca
901 gacagccgag acgtacgagt gcgacgccgt gtggccagcg tgggggcatg cgtcggaaaa
961 tcaccgccta cctgcgatt ttgcagacgt gaagaggaaa acaatttga ttggaccag
1021 cccgcaagcg atgtctgcgc tggcgacaa gatcggaat gccgtcctc ctacgtccgt
1081 caacgtgcc tgtgtgccct ggtaggtga gaccagaag cccaagcgc cagacacaca
1141 gccgcacagc aaacacggc gatcgatata tccacccac tccacacac gagaatctat
1201 gcattgtct atattgtat ctgtatata atatatata acgtatgtt atatatata
1261 atatatata gcatgttaa atgggtacgc cgttcagag ccgtggccac agaaagacag
1321 gcattgtgg agttgtccg atgaactat caaacaagtc gtgaactgg cttttctc
1381 ccgtttga catcttctc gacttttga cgtgtgacgc atcaagaac acacacac

— FROM FIG. 24D(6) —

FIG. 24D(7)

1441 tcaaaatata tglaaatag tatatgtatg catttgiacg tatatatata tatatatata
1501 tatatatata tatatatata ttgcttgtat tatetagtat tatgtttgag agtggttagga
1561 ccttcattgt tatgtatata gcggggactg ctagtgtgtt ttgtgtgtgt catgtgcgag
1621 ttccttgcg acgaaaactg cagtattctt cagttatcca gtccttgcg aatttgaatt
1681 gaaacacggc agetaaatca acaggggtcg catgeatgtt cccgtgagga aagggtgact
1741 tagtcggctg ttcccttgtg caatgatgcg caagtcgalt caacagagtc caacgtctac
1801 gatcgtggat tcagagtcca ggactacgtg acgttcagga acgcggccgt ctgcagctt
1861 tgaagaaaac gtgtcaaacg gagctgtatg caaacctctg gtaaacgacg gtgtgaaagt
1921 tctctttcc gtacttctgt tgcctttcc ctacattgt tgcgtttct gtgttgactt
1981 tgccttctt geatttctt ctgttttta tgtttcagg catggacgtc actgtggacc
2041 tgagtcaagt cgacccacac aaaggccgtg cgcagcagac actgcagctt geatgcgtgc
2101 agtcggccaa ggatgtaggc catgccaaa gtttttcc caggaaaagt ggatttgc
2161 cggaatgca agtgaatata cgagagagcg ctccggccca taggtcgcca tccgttctc
2221 cgtcaaacca ctgtttcact tctctctag gcgttatgtg gtctctatat acgeatctat
2281 ctatcaatcg tgtctatgtt ctgggacgcc gccggctgt ctagaacggc aatgtatgca
2341 catacgcaag atgcctctga aggcggccaa ggacgtgcag tcaattcgtg ctacagaccg
2401 agattcatag atgcagatcc ccacagagat acacctgcgc atgccaaagc acacacgcct
2461 atctatata aaaaatacat atagagaggc ctctctagac tcacatata atatatata
2521 atgtaaatgc atataaatag atgcgcattgt tagaaggctt ttgtacgtg cctgtggacg
2581 catttgcct ttcgttaca tcaggctctg gactgttgcg cgaaaattgg atatcccggt
2641 atgattaagg cgagtgaagg agggggcgcc aaaggcattc gtgcagtcac gaacgcagag
2701 gaggtcgccg acgcgtatcg ccagggtgtc aacgaagtc aagggtctcc agtgttgc
2761 atgcgcattg tctccgattg cagggtcgtt atttctctt ttgtcgtgc tccacctt
2821 cgcgtattg tctttccat tgccttagct gtctccgtt tgcctcatt cctctctt
2881 cgtcgcgtc tctgggtca tgcgcgtgt cgcacgtcg cctctgtcaa gacgcaggtt
2941 ttctaccca cctcgcgtc gacgagcgcc gcgaaactct tgaagagctg agcggctgtc
3001 tgggtgagag aaaatacat ttgcgtctc cgcgaggctt ccaggctacc aggggtcggg
3061 tcgaacgaag aggttccacg tggaaaacga gtgccgtcga ctggtggcgg tctgttct
3121 tgcgcgggg gcttcgctt tgcgggggtg gctgcttct tggaaactcg tgcctagtcg
3181 tglgaagtga acacgaacgc gtctcctc accctgggaaa caggcggaaa cgcgaatgtg
3241 gagatccgt cgaagggtg aacagacagc atttccagcg aagaagctga gaagcagacc
3301 ttctcagtt ccggtccat cgtgtcacc cctcacaact tgcgcgtgt gtacagacac
3361 ctggaggctc agctcttggc agacaagtc gggcgggtcg ttctgcctgg aagtcgggac
3421 tgcctaattc agagaagatg ccaaaaaac attgaagaag gcccgctgt tgcagctct
3481 cccgaggctg ttctcaaat ggaggacgtt gctgcggga tggctatggc ggtgagtgtg
3541 agcaaataga gcttcacgca agttgccgtg agaaaactga atctccatgg gatgccatt
3601 tgaagctca caggaaacgc taaagctaca tgccttga cgtttccct cggacgcca
3661 gtacacaag agtaccctt tactccgaga tgaccgctt acatagaagc atatagtcgt
3721 atattcagat acgcctgat gcttgggtat gtccagtgc acctacgtat atacacagac

— FROM FIG. 24D(7) —

FIG. 24D(8)

3781 ggtatitgc atgegacttt atagtccaan tgtgtacaca tccattaaaa tatacatata
3841 tgtatatata tgtatattta tataratgcg ratgeatgta taccitcgta gacgtgtgtg
3901 tgtgtgtgta catgtgtggc cagcgggtata caggtacaca tgcattgcag gattgggttt
3961 ctgttttatt ttcgtttgcag gtgggggtatg agaatgcggg aacatgtgag ttttgtacg
4021 accccaaaaac taccagttt gcgtttttgg aggtgaacgc gcgcctccaa gtagagcagc
4081 tcttcacaga gtgcgtcggg gacttcaacc tcccggcggc gcagcttcag gtatcgcctt
4141 acgcagccctt cttaaaaag gcgaaaagaa cgtctcgttt tgccttgtt taccggccc
4201 acggcctcgt tgacacagac tcaittgaac acaaatataa acgatacaca attccatata
4261 tatatatat atatatatat atatatatat atatatatat atatatatat
4321 ctgtatgtag tataggata tatgaagata accacaaagt acctctatgt atggatacat
4381 acgttcatgc gttatcttt gttatgtgc atgcgagagt gtatcgtgcg tctgtgtgtg
4441 taggctaggt gcaactgtca gtaggtgcct gcatgatac taaatatata gatttacata
4501 cttttgcctg cctgtcttc tctgccaca ctttatacc acatatatat atatatatat
4561 atatatatat atatatatat atgaatatgc gtgattttc tggcggtgt gtatgcgtca
4621 tccgttggtt tggagggagc gggaaagcga tgcgcgcgtt ttttctgtt tgcctttct
4681 tccaggttg cgttggggat cctgatcat gacatcccag atatcaaggc ctacttggac
4741 tggcgggcca gcaacaagcc cgttggaaaa cacatcatg cagctcggat aacggcggag
4801 catgcagaag aagttagctg ttgttccca cgcactcagc ggagtcgtt ttctgtcgtt
4861 tctttacctt cgtcgcgaat cctacatggg caaaacgtcc gcatacccc cttctgtgt
4921 gttggtgtat ctatcagtt tcatgtctt cgttccgtgc gtatcgggtt aactgtacgc
4981 cgttgcctt ccagtcata acgtcgtgtc ttccagctt tctttctt tctctgtt
5041 cgtgtctgcg tctctactt acgttgtgt acccttcca ttctgttat cgtgtctcg
5101 gtggatctc gtttatcgc gtgcagagag agaggaggtc ggtaaacgag tgacaaacac
5161 gggaggtctg ttgtcactc cgtgaatggt ctttgcgtt tctgaacgag gcgcgggaatg
5221 cgtctttgc actgcattc actttctt tctcgggtca tgcgcgcag cagtccttc
5281 gaccgacagt cggcctcgt cagagctca cgttgcgcc gtgcgcctt gtttgggggt
5341 attttcat cggcagcaag gtgaggaagc cgggaagatt ctgagttt ccgacaggt
5401 ttgggaacc ggaaaactgc gagaagaca gcgagacagt gtccgaggg aattcttgc
5461 tggctccaaa gcgtcagcgt cttactcag tggatggaaa cctcattca gacttaaac
5521 cagagacgc accagacga gttctctgt ttctcgtt cttctgtct tgaattcac
5581 tgcctctc gaacgcgagt cgtcggctc acctctctt gtccctgcc acttggagag
5641 aggtgaacaa gttcgttgg cgtccagag gactctctg cctgtgcct tactgtcgt
5701 ctggtgtctg ggcaactgt ggctctgtca aaaagcttt ctcctccgac gtttgcctc
5761 ccttcacagg gaaacatcca cgcgttcaac gacgtcagt tccgacatc cttgcacac
5821 gggaaggtag gaaggaaggc aagaacgagg acagagaacg ctccgagaga gagagcgaaa
5881 cggagacaga gaaagagctt ccaaggcaga caccagatg gccgcgagga acgagagaca
5941 gacgaagagg aagggagggg caacagggga agaccaaggg agggagagag gcgcaatgca
6001 agagtacga gggagagaag gagagaaacg caggagggga cgcaggtgc aggaagaaaa
6061 acattgcgtg ctggggtat cagagaagag agtgaccgca tgcattgctg tctgggtgcc

FIG. 24D (9) FROM FIG. 24D(8)

6121 cgatcttggc tgaatatgag tgactgcaca cgaagagaga agagaagaga aaagaggaaa
 6181 aaataaatgt ggacgtgtga atgacctga agacaggggg acgaaaattc tcttggcgga
 6241 cgtgagagcg aggcctgaaa aagcgaccaa gagactcgcg acttgacgtt tggcattgt
 6301 tcaattgcag gacagacgag aagctgtcaa acacatgggt ctggcgctca aggacatgac
 6361 aatccgaggg gaactgagaa cgaatgtaga ggctctgac aagattctgg aacatctga
 6421 ctctgttaa gcatcttcg tgcacttag ccttagacc acaaatcac cagcgctctg
 6481 tgcatacag aactcacat cacagtcac atggaaatcc cgcgcctga tatatatata
 6541 tatatgaaa tatatgaaa tatatgata tatatatata tattgtatg tatggcagca
 6601 cactgtctct gtaatgtat ttgtaagtc atttgcact cggcgctccg gtcctcagtc
 6661 gtgggtatac gtgtaaagt cctttatag acgtgagtg tgcctgtgt ccttgaatc
 6721 tgtattctt cgtggagatc tgtgtgtgt gacagctcg tgtgggtga acccgagaa
 6781 gcgctttct gcgagttgt attactaag actcctctt gctctggtg aacagcgatg
 6841 tattgtctga ggcgcgggt gagaatgat gtcgaaacc atcccggtta aagggtgacg
 6901 cctgcgtgca ttagttaa atgttctt tctccagag caatgaaacg cacacgacat
 6961 ggctg

FIG. 24D (10) — FROM FIG. 24D(9) —

LOCUS AF157614 393 bp DNA INV 10-NOV-1999
DEFINITION *Cryptosporidium parvum* acetyl-CoA carboxylase 2 (ACC2) gene,
partial cds.

ACCESSION AF157614

VERSION AF157614.1 GI:6164689

KEYWORDS

SOURCE *Cryptosporidium parvum*.

ORGANISM *Cryptosporidium parvum*

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Cryptosporidiidae; *Cryptosporidium*.

REFERENCE 1 (bases 1 to 393)

AUTHORS Zuther, E., Johnson, J.J., Haselkorn, R., McLeod, R. and Gornicki, P.

TITLE Growth of *Toxoplasma gondii* is inhibited by
aryloxyphenoxypionate herbicides targeting acetyl-CoA
carboxylase

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)

REFERENCE 2 (bases 1 to 393)

AUTHORS Zuther, E., Johnson, J.J., Haselkorn, R., McLeod, R. and Gornicki, P.

TITLE Direct Submission

JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA

FEATURES Location/Qualifiers

source 1..393

/organism="Cryptosporidium parvum"
/db_xref="taxon:5807"

mRNA <1..>393

/gene="ACC2"
/product="acetyl-CoA carboxylase 2"

gene <1..>393

/gene="ACC2"

CDS <1..>393

/gene="ACC2"
/codon_start=1
/product="acetyl-CoA carboxylase 2"
/protein_id="AAF04495.1"
/db_xref="GI:6164690"
/translation="SSGGGGKGIKRLCSSMEDLESNYRQVINEVKGSQ
VFVMRAVVKCRHLEVQVLGDYGDVFALSTRDCTIQRRHQ

FIG. 24D (11) — FROM FIG. 24D (10) —

KVIEEGPVTIVSQEIVKELELSAERMCKAVGYSSAGTVEFLY
DIERSCIAFLEVNARL"

BASE COUNT 129 a 54 c 104 g 106 t

ORIGIN

1 agctcaggag gtggagggaa aggtatccga ctctgcagtt ccatggaaga cctagaatca
61 aattacagac aagttataaa tgaagttaaa ggtagcctaag tatttggtat gcgagcagtt
121 aataagtgtg ggcacctaga gggtcaagta ctaggagaca aatatggtga cgtgttcgca
181 ttgagcacia gagattgcac aatacagagg cgtcaccana aggttataga ggaaggggcca
241 gtacaattg tgagicaaga gattgtaag gaattggagt tatctgcaga gaggatgtgc
301 aaagctgtgg gttattcatt tgcaggaact gttagaattc tatatgatat tgaacgtta
361 tgtatagctt ttctagaagt taatgccaga tta

TO FIG. 24D (12)

FIG. 24D (12) — FROM FIG. 24D (11) —

LOCUS AF157615 393 bp DNA INV 10-NOV-1999
 DEFINITION Plasmodium falciparum acetyl-CoA carboxylase 1 (ACCI) gene,
 partial cds.

ACCESSION AF157615

VERSION AF157615.1 GI:6164691

KEYWORDS

SOURCE malaria parasite P. falciparum.

ORGANISM Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium

REFERENCE 1 (bases 1 to 393)

AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.

TITLE Growth of Toxoplasma gondii is inhibited by
 aryloxyphenoxypionate herbicides targeting acetyl-CoA
 carboxylase

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)

REFERENCE 2 (bases 1 to 393)

AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.

TITLE Direct Submission

JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
 University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA

FEATURES Location/Qualifiers

source 1..393

/organism="Plasmodium falciparum"

/strain="FVO"

/db_xref="taxon:5833"

/country="Viet Nam"

/note="not cloned; isolated from US soldier evacuated from
 Vietnam to Fort Ord; supplied by J. Barnwell"

mRNA <1..>393

/gene="ACCI"

/product="acetyl-CoA carboxylase 1"

gene <1..>393

/gene="ACCI"

CDS <1..>393

/gene="ACCI"

/codon_start=1

/product="acetyl-CoA carboxylase 1"

/protein_id="AAF04496.1"

FROM FIG. 24D (12)

FIG. 24D (13)

/db_xref="GI:6164692"

/translation="SQGGGGKGIRKVENEYEIKKAYEQVQNELPNS
PIFLMKVCNNVRHIEIQVVGDMYGNVCSLSGRDCTTQRRFQ
KIFEEGPPSVVPYPIFREMEKSSIRLTKMIKYRGAGTIEYLYD
QINKKYFFLELNPRL"

BASE COUNT 156 a 39 c 72 g 126 t

ORIGIN

1 tcacaagggtg gtgggtgggaa aggtattega aaagtggaaga atgaatatga aataaaaaaaaa
61 gcatatgaac aagtacaaaa tgaattacct aattctecta tattttgat gaagggttgt
121 aataatgtaa gacatatga aatacaagtt gtgggtgata tgtatggaaa tigtgttct
181 ttaagtggtc gtgattgtac tacacaaaga agatttcaaa aaattttga agaaggacca
241 ccategttg taccatatcc tatatttega gaaatggaaa aatcatctat acgattacct
301 aaaatgatta aatatagagg tgetggaact attgaatatt tgtatgatca aataaataaa
361 aaatatatt tcttagaatt aaatccaaga tta

— FROM FIG. 24D (13) —

FIG. 24D (14)

LOCUS AF157616 393 bp DNA INV 10-NOV-1999
DEFINITION Plasmodium knowlesi acetyl-CoA carboxylase 1 (ACCI) gene,
partial cds.
ACCESSION AF157616
VERSION AF157616.1 GI:6164693
KEYWORDS
SOURCE Plasmodium knowlesi.
ORGANISM Plasmodium knowlesi
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 393)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Growth of Toxoplasma gondii is inhibited by
aryloxyphenoxypionate herbicides targeting acetyl-CoA
carboxylase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)
REFERENCE 2 (bases 1 to 393)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA
FEATURES Location/Qualifiers
source 1..393
/organism="Plasmodium knowlesi"
/strain="H"
/db_xref="taxon:5850"
/country="Malaysia"
/note="supplied by J. Barnwell"
mRNA <1..>393
/gene="ACCI"
/product="acetyl-CoA carboxylase 1"
gene <1..>393
/gene="ACCI"
CDS <1..>393
/gene="ACCI"
/codon_start=1
/product="acetyl-CoA carboxylase 1"
/protein_id="AAF04497.1"
/db_xref="GI:6164694"

— FROM FIG. 24D(14) —

FIG. 24D(15)

/translation="SQGGGGKGIRKVENEEI KKA YTQVQMELPNSPIFLMKVC
SNVRHIEIQVVGDMYGNVCSLSGRDCTTQRRFQKIFEEGPP
SVVPPNIFREMEKASIRLTKMIKYRGAGTIEYLYDQEKQTY
FFLELNPRL"

BASE COUNT 138 a 69 c 91 g 95 t

ORIGIN

1 tcacaaggag gaggggggaa aggtattcgg aaagtggaga acgaagaaga aataaagaaa
61 gcctacacac aagtgc aaat ggaattaccc aactcgccct tctttctaat gaaagtctgt
121 agcaacgta gacacatcga aatacaagtt gtgggggata tgtatggtaa tgtatgcctc
181 cttagtggaa gagactgcac gacccaaagg aggttccaaa aaattttga agaagggtcc
241 ccttcagttg tacctccgaa tatttccgt gaaatggaaa aggcattccat acgtctaaca
301 aaaatgataa aatatagagg tgcgggaact attgagtatt tatatgacca ggagaagcag
361 acttatttt ttctcgaatt aaatccctga ctg

FIG. 24E

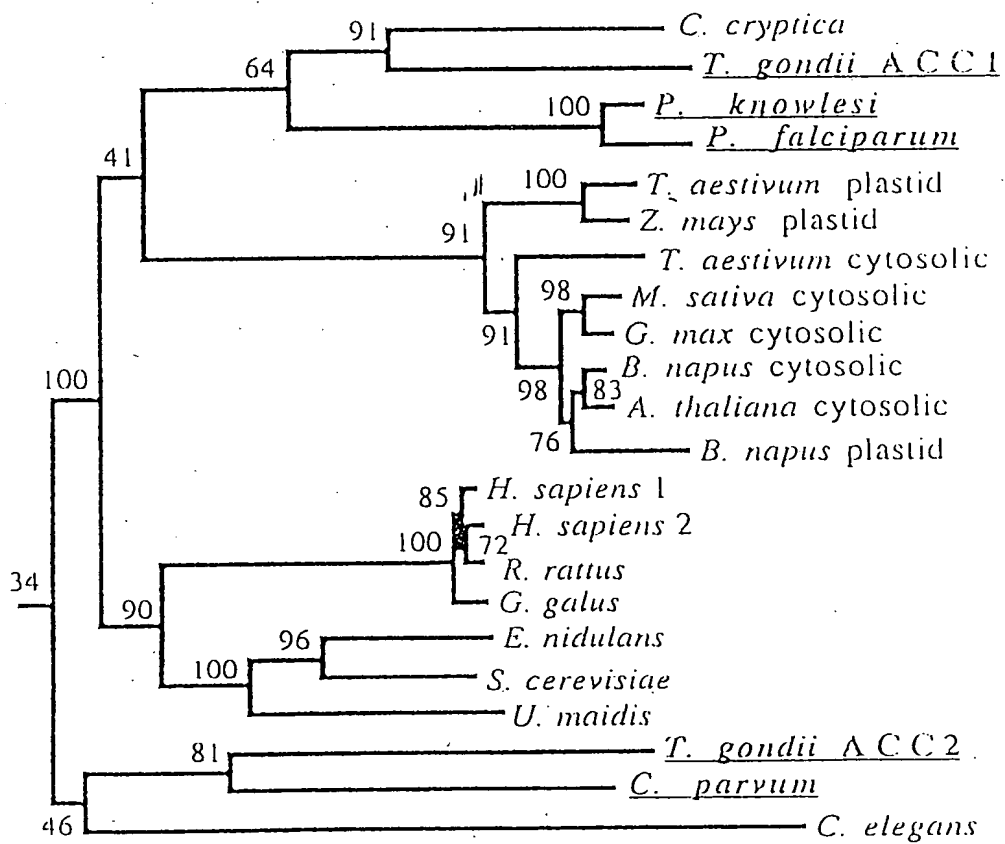


FIG. 24F

Aryloxyphenoxypropionates (fops)

Haloxypop: $X=CF_3$, $Y=Cl$

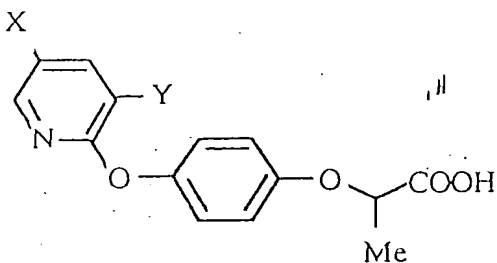
Haloxypop methyl ester

Haloxypop ethyl ester

Fluazifop: $X=CF_3$, $Y=H$

Clodinafop: $X=Cl$, $Y=F$

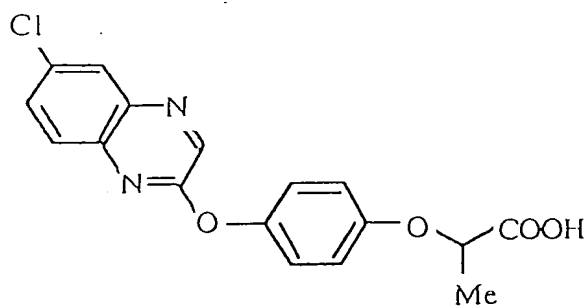
Topik, clodinafop propargyl ester



Quizalofop

Targa, quizalofop ethyl ester

Agil, quizalofop 2-isopropylideneaminoxyethyl ester



Cyclohexanediones (dims)

Sethoxydim: $X=CH_2CH(CH_3)SCH_2CH_3$, $Y=CH_2CH_2CH_3$, $R=CH_2CH_3$

Cethoxydim: $X=C(SCH_3)CH_2$, $Y=CH_2CH_3$, $R=CH_2CH=CH_2Cl$

Clethodim: $X=CH_2CH(CH_3)SCH_2CH_3$, $Y=CH_2CH_3$, $R=CH_2CH=CHCl$

